

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 25, 2003, 08:33:12 : Search time 1051 Seconds
(without alignments)
12857.212 Million cell updates/sec

Title: us-09-831-000-1

Perfect score: 40000

Sequence: 1 gacgcgggaaacgcgaggg999.....acctatgataactcgttt 40000

Scoring table: OLIGO-NUC
Gapop 60.0 , Gapext 60.0

Number of hits satisfying chosen parameters: 378376

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GB_VI:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40000	100.0	133719	1 AF083501	AF083501 Macaca mu
2	10772	26.9	130733	1 AF210726	AF210726 Macaca mu
3	7957	19.9	10595	1 AF029302	AF029302 Rhesus ma
4	3804	9.5	3804	1 AF087411	AF087411 Rhesus ma
5	475	1.2	475	1 AF159033	AF159033 Macaque g
6	331	0.8	395	1 AF159041	AF159041 Macaque g
7	106	0.3	320	1 AF159040	AF159040 Macaque g
8	80	0.2	2708	1 AF204167	AF204167 Macaca ne
9	71	0.1	475	1 AF159031	AF159031 Macaque g
10	56	0.1	336	1 AF159034	AF159034 Macaque g
11	50	0.1	475	1 AF159032	AF159032 Macaque g
12	48	0.1	336	1 AF159036	AF159036 Macaque g
13	48	0.1	336	1 AF159037	AF159037 Macaque g
14	47	0.1	336	1 AF159035	AF159035 Macaque g
15	46	0.1	3144	1 SHIDNAPOLA	L24487 Pseudorabies
16	41	0.1	336	1 AF159038	AF159038 Macaque g
17	38	0.1	475	1 AF282937	AF282937 Mandrillu
18	38	0.1	475	1 AF282938	AF282938 Mandrillu
19	38	0.1	475	1 AF282939	AF282939 Mandrillu
20	38	0.1	475	1 AF282940	AF282940 Mandrillu
21	33	0.1	130733	1 AF210726	AF210726 Macaca mu
22	33	0.1	133719	1 AF083501	AF083501 Macaca mu
23	32	0.1	454	1 CRH251574	A251574 Chloroceb
24	31	0.1	523	1 A1237372	A1237372 Caprine h
25	29	0.1	395	1 AF159039	AF159039 Macaque g
26	29	0.1	469	1 AF031811	AF031811 Bovine he
27	29	0.1	3638	1 AF005477	AF005477 Kaposi's
28	29	0.1	108873	1 AF318573	AF318573 Bovine he
29	29	0.1	133661	1 U93872	U93872 Kaposi's sa
30	29	0.1	137508	1 KSU75698	KSU75698 Kaposi's sa
31	27	0.1	480	1 AF031808	AF031808 Bovine ly
32	27	0.1	1295	1 AF327830	AF327830 Bovine ly
33	26	0.1	475	1 AF005478	AF005478 Retroperi

34	26	0.1	3554	1 AF204166	AF204166 Retroperi
35	23	0.1	475	1 AF250880	AF250880 Pan trogl
36	23	0.1	1297	1 AF327831	AF327831 Ovine her
37	23	0.1	1339	1 AF275657	AF275657 Badger he
38	23	0.1	6165	1 AF376034	AF376034 Badger he
39	23	0.1	184427	1 EHVU20824	U20824 Equine herp
40	22	0.1	171096	1 AV037858	AV037858 Cercopit
41	22	0.1	949	1 AF292063	AF292063 Identif
42	21	0.1	3623	1 AF283477	AF283477 Caprine h
43	21	0.1	12708	1 AF033822	AF033822 Walleye d
44	21	0.1	12708	1 TYCGAG	L41838 Walleye der
45	21	0.1	130608	1 AF005370	AF005370 Alcelaphi

ALIGNMENTS

RESULT 1	AF083501	133719 bp	DNA	Linear	VRL 26-JUN-2000
LOCUS	AF083501				
DEFINITION	Macaca mulatta rhadinovirus 17577, complete genome.				
ACCESSION	AF083501.3				
VERSION	GI:8714565				
KEYWORDS					
SOURCE	Macaca mulatta rhadinovirus 17577				
ORGANISM	Macaca mulatta rhadinovirus 17577				
REFERENCE	Seattles,R.P., Bergquam,E.P., Axthelm,M.K. and Wong,S.W.				
AUTHORS	1 (bases 1 to 133719)				
TITLE	Sequence and genomic analysis of a Rhesus macaque rhadinovirus with similarity to Kaposi's sarcoma-associated herpesvirus/human herpesvirus 8				
JOURNAL	J. Virol. 73 (4), 3040-3053 (1999)				
MEDLINE	99174001				
PUBMED	10074154				
REFERENCE	2 (bases 1 to 133719)				
AUTHORS	Seattles,R.P., Bergquam,E.P., Axthelm,M.K. and Wong,S.W.				
TITLE	Direct Submission				
JOURNAL	Submitted (11-AUG-1998) Division of Pathobiology and Immunology, Oregon Health Sciences University/ Oregon Regional Primate Research Center, 505 NW 185th Avenue, Beaverton, OR 97006, USA				
REFERENCE	3 (bases 1 to 133719)				
AUTHORS	Seattles,R.P., Bergquam,E.P., Axthelm,M.K. and Wong,S.W.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-JUL-1999) Division of Pathobiology and Immunology, Oregon Health Sciences University/ Oregon Regional Primate Research Center, 505 NW 185th Avenue, Beaverton, OR 97006, USA				
REFERENCE	4 (bases 1 to 133719)				
AUTHORS	Seattles,R.P., Bergquam,E.P., Axthelm,M.K. and Wong,S.W.				
TITLE	Direct Submission				
JOURNAL	Submitted (26-JUN-2000) Division of Pathobiology and Immunology, Oregon Health Sciences University/ Oregon Regional Primate Research Center, 505 NW 185th Avenue, Beaverton, OR 97006, USA				
REMARK	Sequence update by submitter				
COMMENT	On Jun 26, 2000 this sequence version replaced gi:5508840.				
FEATURES	Location/Qualifiers				
SOURCE	1..133719				
repeat_region	/organism="Macaca mulatta rhadinovirus 17577"				
CDS	/mol_type="genomic DNA"				
	/db_xref="taxon:93534"				
	1..840				
	/note="partial terminal repeat"				
	/codon_start=1				
	/product="R1"				
	/protein_id="AAD21330.1"				
	/db_xref="GI:4494908"				
	/translation="MFTVLEMLQPPSVVELLPKLTSTVPTCPHEDDTYLLTGRCT				
	STANDSTONFNNNTLVKSGNFTGRVLSVTPNATISDRVACQRTTTRSNIDFRVS				
	SSRLTIOERSSGYTANNRVRGCVSGGVTLRNVFHLNGTAVINHTTTNHTTV				
	LTERTGTYPCSAFIGNEKFSQRTINVEFTSFTRKPTNDIPNESHFNKTOIOOTASV				

CDS

OHPEKVVVPSVPSFISGVLITGIAISLINCHLFTTCNSENSESTSYASQTSYIOPSH
NORNTNCSRHRTTKNAHOESIEELPNQHSSETSCOLVILEVKNVAIDSPQNTI
NEMEQYDDVVVKNIEQTSYEDNVEMHDSIDINPNFNYSGLILEEVEDEVYENLEN
OYHGILLENLDHNEYNHLNEMIMQYDWLE"
complement(2692..3258)
/note="ORF 2: similar to Kaposi's sarcoma-associated
herpesvirus ORF 2"
/codon_start=1
/product="dihydrofolate reductase"
/protein_id="AAd21331.1"
/db_xref="GI:4494909"
/translation="MDITVNCIIVAVDEOLGIGKNGTMPRLNEMMYFOKMTSPSV
VGEKNVVMGKRTFSIPEKRPVLRNINILSRLEKRPFAHFLARTLDIAFMYR
OYKKEQJLNTVMYIGKSYVESVLTNCKPLKYLIRIMESPCDVFPFSINTEYTM
SEIPKQDNFEENGIRKYKFOYKFNK"

CDS

3676..5613
/note="ORF 4: similar to Kaposi's sarcoma-associated
herpesvirus ORF 4"
/codon_start=1
/product="complement binding protein"
/protein_id="AAd21332.1"
/db_xref="GI:4494910"
/translation="MTFKLFLPLFLHAIIMYVHCDECKPHEFTYKVSNTBKLYS
GETALICRPGVNTKIITTECLONGTMSPTNPPCDKRCPTPADLILNGAVHIGD
NAKGSNISYECNCGVDLIGSNVRCTLODPENMNSPEVCIQKICIRAYEHG
DYLPMQDYNNGDATTFCOSLSYTLVGSTTLVCTISNKRNSFPICLMLVCSPIDN
GITDGLSRYNHGSITVCKSDGYNIVGPELTCTNTWPEIKVCYLVTNNPOTPM
PETPEPTPTDYOKINLSTAKATTPNAFVTTVVSPKDDVTGVKPHFERMVAEN
DEKETSVASVELICRPGFTKQSTVSECLNSGWTAPNAKCHRRCKPTEPOLNIGE
YIVSGEAPKFGTNTITKYNCGYOLGSMVIGLKDCLKDVTMWEKAPKIDIECK
PPQITNGKHYKDFYQYLDIYVFCNMRDSELDVDEMTCTISNTNKCIPPCEDITC
SAPNIAHKLITGSSSYKKGOSVITGCEGTGLIGSELSTCKDSSMDPLPTCPAV
SMPSOTPEKTKPNTPEAKPNTPNVGTHTPKPPPNPIAPPMKMRHVVL
LEASVALFLVLAALYCCFLK"

CDS

6045..9443
/note="ORF 6: similar to Kaposi's sarcoma-associated
herpesvirus ORF 6"
/codon_start=1
/product="ssDNA binding protein"
/protein_id="AAd21333.1"
/db_xref="GI:4494911"
/translation="MASKNGOPLDNOGSRAPIGAGGYVAYAKODEPFAEASILG
NRPSSGVFSLPIYGLVHEHPEPLTVKAAKKVDTTALVKNCEHREIVYFNAST
FRPYDGTGMLNCEEARALRGYTOPIFERGPHSITWNPBECQIDKDEMTAGVYTE
GFERLMRGCLVPAFVTOVOOIAGRQAFLVDEDLFAPGHMRPRFYHDAVYL
YDLETSIAQALRLKDVAVIHAIEKQPMODHYKIAKIVQAKQFSTLPKTDGSSM
IVDSVVALALSYCGMFECPDACELNDSMPFDCDSEARVNALEMSAQAV
HVAQGLFPAANSVLYLTQYKQAPRGOKGDVNVNSEFLQHGFLNEATIKENGSEAF
KGVPSNALDSSFTPYHLYAASPSHLAKLYCMOFLQHHKSTNOAFNWHVGT
AANSKCTLCGNTPATCLNTLFLRLKDRFPAVTPPQRDPVVTGAGTFNDELIG
NFASRDEEDGNPADEHKYTWQLCQTVTEKLSAIGITEDHNMNLINIOSELR
VEKIDISIVDEVMKFMVSMIKNNFNREHYSVHIIQFCCNVWQAQCAVFLVLY
KSLMIIDICLPCMIEYEDONPANGILPEMLKMFOTLWNEKACLDLGVGCE
LKIYHRDCEDFPDAGSNGIMAFKMQVIRARMAVVPKSIKINRIITFSNTGSE
AVQSGVYKPGTGRDYYVAGPYMKTLNHLARPDTKTAALYIHKISQNTKYVAK
DVPDELAELIYKTNLSLAFEBETVLDVDPDSLSIKUNGAIIAACGDIQYAT
TULHCTFVLQTIIDEEYPHVLGSAIAIPVAYLAIRGRTALTVOGTARQVPAAGRL
RPVITPVMVVKYTGCVNGNNVNFHCGNLGYPAGRGVDRNLPESSPEFKTKYSAALRK
RHVMATPIIDRLIKAAQOTISTFEASVRSVQALLKEDKNPNLKSYLELHLIG
KGCODLSEEDVOYLYGDYCM/LDEVLFLLDNIAGOSGVPWTEADGALIEDQDADLO
FVDSDDIATASCPPEBOLPTPSAGALLAGKKRKNALISDLI."

CDS

9468..11528
/note="ORF 7: similar to Kaposi's sarcoma-associated
herpesvirus ORF 7"
/codon_start=1
/product="transport protein"
/protein_id="AAd21334.1"
/db_xref="GI:4494912"
/translation="MARLAALYAQLSALAVDLVTFADPRSIDGARILTKTQIEN
LNRDLPLLRONSVEYTSLSLEVEHLAKNIEDKLGELERSLRQYSREHEFTLHR
PECHYHSVTFQFQGGILDVNMCILINDVELLCRSGFYVICANEAELVAVT
LSTLRGISPIRHPDLVYSPVOCVLCRIEILVPRNGSSSLAVIADRHDHLCCKYRAE
PIHGLFETELSQLIKTKRSDATQHGVRSSADOLRESSLAIDQHNIFKRYASIME

CDS

LSNLIYNAAGCTGLOGTENECGSAQRILTFHADNHEHALTPKLSATHEYDCRPD
PESLFCGGLFESITDITINALSDGCVTFPQDQATNWRKONELFTPLNLSLRGSA
GSOQKPAPESEPTTVAATAASVDIKQYRREOQYKVARQGFKECTLOQSAVL
ANALCMRWGVAAGEASELVNHFLLRRFVALPWEAKRSDQYLFENSKYIKNSLY
OALSRHEHIEITLOFGLITGTLTROSLEPPAPVAAAOCEAGMPLPHMVLVEM
IMPOIOPKMDIOOTFNRYOJLEPGLNVAOKSAWCFIHELIVSVLRYNTEKTLRIF
SLAREKLSINIDVAGLISGLYLTVEQDAPLVLIQNTGMIKFDLXALLYHHLQSDG
HDDN"

CDS

11515..14004
/note="ORF 8: similar to Kaposi's sarcoma-associated
herpesvirus ORF 8"
/codon_start=1
/product="glycoprotein B"
/protein_id="AAd21335.1"
/db_xref="GI:4494913"
/translation="MAMTRKRLRLANVIAIIGTAGENVYTPKGAATTAKPPPG
SPTPEPMPRAEAFKFRVCSATGELEFRLEKTEGTEKTOQESILWMEKKNIV
PHIFKVRRYRKVATSVTVYRGWETAVMGKQIVAPVOYEINHDYTYOCSSRVN
VNGIYNTYDTRDFNTQYVFLQPBELTNIQYFESQVLYTTPGPGCIYVRRTVNC
EIVMDIARSABEYSTVTAIGDTEVSPFCHNDSTCVSAEKTENGLCARVLNTIYD
FATROPTEETRVFADSGEYVSWKADKRSACALTLTKTEPRAIQTTHASVYHAN
DVTATFETPLSQVNTMGTYPCLDINATIKLSDTATNGSDQYETEGLF
LLMOPLTPLSLADEMRELNGTPAPPTTSTANRYRSVGTNEQATDIDLAQLOFAY
DKLRASINKVLEELSRAMREQVRLTVMWYELSKINPTSVMTAIGRVSAKFEVDAT
SVTDQAVDQASVSTHKSLRTSTICYSRPPRFRINSTTILFKGOLGPRREIITD
NOVEKECTCEHTFASVYTYIKDYVYKATINSEITLGTFLIANSPENIDERV
IELYSRAEKRLSGSVFDEIEMREYNTYTORLAGREDEDIDNTIDNRRLADSEIV
ADLGVGTGYNVAVASVITLESISVGEINFIKSPFGMLMVLIVAAVLIVFALNR
TNIAIQAPILRMVYPIDIKMOPSGGVSDQEIINILAGHOLQOEEERRRLDEQORSAS
LEFRASDGIKREFRGYKPLENEAQEYEMSK"
14122..17166
/note="ORF 9: similar to Kaposi's sarcoma-associated
herpesvirus ORF 9"
/codon_start=1
/product="DNA polymerase"
/protein_id="AAd21336.1"
/db_xref="GI:4494914"
/translation="MDFPNYILGPRGPRPHSRIGDAPAPAGAGAVOPPPVCRILPA
CIRTPAGAGMTLVITIPPPYTFENKARDVLLANRSKWTADKRPVAPDPDOSITF
HAYDVETTYADRCANVPSRQNDIISGVYKILGTEGTSVCVNFQOYEVYA
KVPAGINVTYHILQOALKNTAGAACGFESTRYRNKILKTYVAEHPVEITLSSGML
STLSRLVACGEVFNVDVARDVRLDHGFTFPMYSCARATPLADARLATAEPD
CSMEDLSVADRSDMPVARIADVIECGGAGFPACGAVTIOISCVFTATREAG
NPNILTSVGCDDPIPTDVLFEPSYEMLYSFRMIDPEVDITGINSFDPLY
ITRASQVLRNLETYKIKTGSIFEVHPRGGGGSFMSVSKITAGIYVPIDMTOCR
EKLISDYKILPTVARQCGCKEDVSYDDIPLFSGSGRAKGSYCVMSVLMVL
LKMFIHVEISIAKLAKIOARVYLTDCQQLAFVSCLEAAARENFILPVPPEGOG
YOGATVINDIGFVDEPLVVDPAFSLYSIOAHNLCSYTHHGBDLHLPLPPDDY
ETVYSGPVHVRHKKRRESILGRLLYWLKRRRIIRRTIAACDPSLTTDLKOLA
IKVTCNAVYGTGVAAGILPCINTAIEYTLKRTMLREMSKYVEALITTEDLTKRGRE
VTARGAFFRVVYGTDSLFACDGYSAEAVSAFCDLDAARTADLPFPKLEKKT
FKCLLLRKHRRKIRGLVLDKVMKMKVDLIRKTACFEVORCAIIDLVLHPDEVAA
RLCLRHPHAYEBGLPAGFKIYVLAASVYLDLNSVAPLEOLFSTELSRPVDYK
TNNPLHAVOYKALSRCELDQVHRIRIYVFPVADAGSKSDIAEHPDVVRQHQPVAV
DLYPRKLHGKANILQCLFGRNADTYVALILNPLNVPKLES"

CDS

17261..18511
/note="ORF 10: similar to Kaposi's sarcoma-associated
herpesvirus ORF 10"
/codon_start=1
/product="unknown"
/protein_id="AAd21337.1"
/db_xref="GI:4494915"
/translation="MLVNLISVLGDMVEVTFHGRFSFVNLTQLQTEFGHGIVARVL
PESLDOLHOFHAFGLVRLKLELPFSSCVALLVPLDGGADARVAPGVLDSSRP
LTVWVNASGRHTIRFCLILFLKPIDLERVAVTVFGNGAGARSGEYTPKPPCAENLGGP
LRVSGEASOTSPHSVAVFPTANVACSLRLQVRSPPDAAHDAISPKYVTFNS
SGGVNCRKASVHTLSRCKTQAMETIYVAPCPNMEIYVGGSGAPVLPFTHTGGRVYVA
DAEKTIQPGSSHEVAVQLITFOOGAARBDLFLVTVGAPELFPVYTPMLLSGCTHL
RLFNFNGPTTIIKDTLVAAPVAAAPCVNVLSSADAPADVLVAPDGLUSINAFTIPVG
FPGVVSACCHVTLIRDNNGVHERMNH"

CDS

18520..19749
/note="ORF 11: similar to Kaposi's sarcoma-associated
herpesvirus ORF 11"

Query Match 100.0%; Score 40000; DB 1; Length 133719;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 40000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATCGGGAAAAACGCGAGGGAGCGGGGGACAGGGGACGGCGTGTGCTGCTTGTGAGACA 60
DB 1 GATCGGGAAAAACGCGAGGGAGCGGGGGACAGGGGACGGCGTGTGCTTGTGAGACA 60
QY 61 CCGGGGTACGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 61 CCGGGGTACGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 121 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 121 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 181 GCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 181 GCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 241 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 301 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 301 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 361 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 361 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 421 AGGGGACAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 421 AGGGGACAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 481 GTAGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 481 GTAGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 541 GTAGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 541 GTAGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 GTAGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 601 GTAGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 661 GTAGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 661 GTAGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 721 GGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 721 GGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 781 CAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
DB 781 CAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
QY 841 AGGACAAAGCAGTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 841 AGGACAAAGCAGTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 901 AGTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 901 AGTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 TTTTCCAGGGAAGGGGTACATGACGCGCAAGTTTACAAAGCCTGCTTAACTGCTTGTG 1020
DB 961 TTTTCCAGGGAAGGGGTACATGACGCGCAAGTTTACAAAGCCTGCTTAACTGCTTGTG 1020

QY 1021 GCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1021 GCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
QY 1081 CTTGCAATACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1081 CTTGCAATACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1141 TCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
DB 1141 TCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
QY 1201 TACAAATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
DB 1201 TACAAATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
QY 1261 TAAATGCAATTTTACATTTTACATTTTACATTTTACATTTTACATTTTACATTTTACATTT 1320
DB 1261 TAAATGCAATTTTACATTTTACATTTTACATTTTACATTTTACATTTTACATTTTACATTT 1320
QY 1321 GTGTTTAAATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
DB 1321 GTGTTTAAATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
QY 1381 TGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
DB 1381 TGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
QY 1441 CACCAATCCCGGAGATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
DB 1441 CACCAATCCCGGAGATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
QY 1501 AGCGAGCAGCAATGGTTTGGCAACACAGCTTATGCGGGGATTTTCTTACGGCA 1560
DB 1501 AGCGAGCAGCAATGGTTTGGCAACACAGCTTATGCGGGGATTTTCTTACGGCA 1560
QY 1561 GACTGTATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
DB 1561 GACTGTATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
QY 1621 CAACAACCGGAGATACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
DB 1621 CAACAACCGGAGATACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
QY 1681 AACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
DB 1681 AACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
QY 1741 CTGCTGGAACGCTTAAAGAAAGCTTGTCTTCAATTTAAAGCTGCTGCTGCTGCTGCTGCTGCT 1800
DB 1741 CTGCTGGAACGCTTAAAGAAAGCTTGTCTTCAATTTAAAGCTGCTGCTGCTGCTGCTGCTGCT 1800
QY 1801 ACGCTACTACAAACATACATATTTGCTTAAAGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
DB 1801 ACGCTACTACAAACATACATATTTGCTTAAAGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
QY 1861 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
DB 1861 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
QY 1921 CTTGATTTACCTTTTAAACCTTAAACGCTTAAACGCTTAAACGCTTAAACGCTTAAACGCTTAA 1980
DB 1921 CTTGATTTACCTTTTAAACCTTAAACGCTTAAACGCTTAAACGCTTAAACGCTTAAACGCTTAA 1980
QY 1981 GGCATAATACAAACAGCTAGTGTACAAATCTGGAAGAACTACCTGCTGCTGCTGCTGCTGCT 2040
DB 1981 GGCATAATACAAACAGCTAGTGTACAAATCTGGAAGAACTACCTGCTGCTGCTGCTGCTGCT 2040
QY 2041 CCGTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100
DB 2041 CCGTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100
QY 2101 TTACAATACGCTGCAACGAGAACTGTAATCATCAATTAATAGTTATCAAGCCAGCA 2160

Db 2101 TTACAAATGCGTCAACGAGAACTGGAATCATCACTAATAGTTATGCAAGCAACAA 2160
QY 2161 GGTACATTCACCCCTCCCAATATCAGCGTTCCAAATCTAATGAATAGTACGCATACCT 2220
Db 2161 GGTACATTCACCCCTCCCAATATCAGCGTTCCAAATCTAATGAATAGTACGCATACCT 2220
QY 2221 ACAGAAATGCTCATCAGAAAGAGATATGAGAACTACCAACCAACACACAAAGTGAAA 2280
Db 2221 ACAGAAATGCTCATCAGAAAGAGATATGAGAACTACCAACCAACCAACAAAGTGAAA 2280
QY 2281 CTGATCTTGCTGCTCAATAGTTTACTGTAAGTGAAGAAATGAGCCCTAGATGAGACCG 2340
Db 2281 CTGATCTTGCTGCTCAATAGTTTACTGTAAGTGAAGAAATGAGCCCTAGATGAGACCG 2340
QY 2341 AGGAAACACAAATTAAGAAAGTATGAGAACAGATATGATGATGTTGTTGTAAGAAATATAG 2400
Db 2341 AGGAAACACAAATTAAGAAAGTATGAGAACAGATATGATGATGTTGTTGTAAGAAATATAG 2400
QY 2401 AACAAACATCATATGAGATATGTTGAGCACATGACATATAGTATCTATATATATCCCA 2460
Db 2401 AACAAACATCATATGAGATATGTTGAGCACATGACATATAGTATCTATATATATCCCA 2460
QY 2461 ATTTTATATCTATGACATGACATATATTTGGAAGAAAGTAAAGTATTTTAAATGAAAC 2520
Db 2461 ATTTTATATCTATGACATGACATATATTTGGAAGAAAGTAAAGTATTTTAAATGAAAC 2520
QY 2521 TAGAAATATCAATATCATGATTAATCTGAGAAATTTAGATCAATGATGATCAATCAT 2580
Db 2521 TAGAAATATCAATATCATGATTAATCTGAGAAATTTAGATCAATGATGATCAATCAT 2580
QY 2581 TAAATCAATTAACATGATAGAAACATATGATGTTAGTAATATATATCTGTTGAT 2640
Db 2581 TAAATCAATTAACATGATAGAAACATATGATGTTAGTAATATATATCTGTTGAT 2640
QY 2641 TTTTAAATTAACATTAACATTAAGGACATTTTGTGTAATCTTATATAT 2700
Db 2641 TTTTAAATTAACATTAACATTAAGGACATTTTGTGTAATCTTATATAT 2700
QY 2701 AAAATTTTTCATATACCTGAAACTATATTTATTTCCATTTCCCTCAAGTTGTATC 2760
Db 2701 AAAATTTTTCATATACCTGAAACTATATTTATTTATTTCCATTTCCCTCAAGTTGTATC 2760
QY 2761 TTTGCGCGGTATCTGATTAACATGCTGATTTCTGTAATTAATTTGATGAGAAATATAC 2820
Db 2761 TTTGCGCGGTATCTGATTAACATGCTGATTTCTGTAATTAATTTGATGAGAAATATAC 2820
QY 2821 ATCAGAAATCAAACTCTCATATATGCGGTAATATATAGTTTAAAGGACACTATATAT 2880
Db 2821 ATCAGAAATCAAACTCTCATATATGCGGTAATATATAGTTTAAAGGACACTATATAT 2880
QY 2881 AAGAACATCTCATATAAAGAGATTTTCTCCAAATACCCAGACCGTTTAAATGTTCTTT 2940
Db 2881 AAGAACATCTCATATAAAGAGATTTTCTCCAAATACCCAGACCGTTTAAATGTTCTTT 2940
QY 2941 TAGTTTGTATGTTCTATATGAATTAAGCATCTCTAGCGTTCTGCTAGAAAGTGTGC 3000
Db 2941 TAGTTTGTATGTTCTATATGAATTAAGCATCTCTAGCGTTCTGCTAGAAAGTGTGC 3000
QY 3001 TCGGTGCGGTGCTACGTAATTTCTGTCAAAATATATTAATTTCTGTCACGAGAG 3060
Db 3001 TCGGTGCGGTGCTACGTAATTTCTGTCAAAATATATTAATTTCTGTCACGAGAG 3060
QY 3061 GCGCTCTTTTTCAGGATGAAACCATGTTCTTTTCCCATATATACCATTTCTTTTC 3120
Db 3061 GCGCTCTTTTTCAGGATGAAACCATGTTCTTTTCCCATATATACCATTTCTTTTC 3120
QY 3121 ACCTACACCGATGCGGTAGACGCTATTTCTGAAATATACATATTTCTTTCTAAGTA 3180
Db 3121 ACCTACACCGATGCGGTAGACGCTATTTCTGAAATATACATATTTCTTTCTAAGTA 3180
QY 3181 GGGCCAAAGCATTTGCTGTTTACCAATTTCTATTTGTATCTAAGTCAACGACATGCA 3240
Db 3181 GGGCCAAAGCATTTGCTGTTTACCAATTTCTATTTGTATCTAAGTCAACGACATGCA 3240

Db 3181 GGGCCAAAGCATTTGCTGTTTACCAATTTCTATTTGTATCTAAGTCAACGACATGCA 3240
QY 3241 GTTAAGTATATGATGATGTTTATGTTGACATGACGGGTTTAAACAGAAATATTTCA 3300
Db 3241 GTTAAGTATATGATGATGTTTATGTTGACATGACGGGTTTAAACAGAAATATTTCA 3300
QY 3301 CAATTTAAACAATTAACACAGTGCATGTACTTACTAATGTATAGTAAAGTATGTA 3360
Db 3301 CAATTTAAACAATTAACACAGTGCATGTACTTACTAATGTATAGTAAAGTATGTA 3360
QY 3361 TAGTATATCATATGCTTTTCAATATGAGACAAAAGAAAATGTTACCTGTGTTAAG 3420
Db 3361 TAGTATATCATATGCTTTTCAATATGAGACAAAAGAAAATGTTACCTGTGTTAAG 3420
QY 3421 CCTACCTGTTTGGATGATTTATGTTTACATATGAAATTAATATATATATTAACGTT 3480
Db 3421 CCTACCTGTTTGGATGATTTATGTTTACATATGAAATTAATATATATATTAACGTT 3480
QY 3481 TTTTACGTAAACATATTTGTAATTTAATCAGCGATGTTATATGTTGCTATACACACA 3540
Db 3481 TTTTACGTAAACATATTTGTAATTTAATCAGCGATGTTATATGTTGCTATACACACA 3540
QY 3541 ATGTTTGCATTAAGACATATGTTATGAGCTTCAATCTTTATTTTATTCAAATTTGT 3600
Db 3541 ATGTTTGCATTAAGACATATATGTTATGAGCTTCAATCTTTATTTTATTCAAATTTGT 3600
QY 3601 TTTAAGAGGATGATATATATTTTAAACAGCATTCAGAAATATAGCGCAACGCTGCTCGT 3660
Db 3601 TTTAAGAGGATGATATATATTTTAAACAGCATTCAGAAATATAGCGCAACGCTGCTCGT 3660
QY 3661 ATATAGTGTATTAACATGACGTTTAACTTTTCTGTTTCTGTTTATTTACACGCGATATG 3720
Db 3661 ATATAGTGTATTAACATGACGTTTAACTTTTCTGTTTCTGTTTATTTACACGCGATATG 3720
QY 3721 TACGTCCAGTGCATGAAACCTGTAACCCGACATTTTACGGAATATGCGGCAAGTCT 3780
Db 3721 TACGTCCAGTGCATGAAACCTGTAACCCGACATTTTACGGAATATGCGGCAAGTCT 3780
QY 3781 AACACAGAAAGGACTTATATATGTTTGGAAACAGCTGAATTAATTTGTCGCTCGT 3840
Db 3781 AACACAGAAAGGACTTATATATGTTTGGAAACAGCTGAATTAATTTGTCGCTCGT 3840
QY 3841 TATGTTACAAATTAACAAATTAATTAACACAGAAATGTTTACAAATGATGCTGTAACA 3900
Db 3841 TATGTTACAAATTAACAAATTAATTAACACAGAAATGTTTACAAATGATGCTGTAACA 3900
QY 3901 CCAATTTTTCATGCGACAGAAAGATGTCACACGCTGCTACTTGTGGAATGAGCC 3960
Db 3901 CCAATTTTTCATGCGACAGAAAGATGTCACACGCTGCTACTTGTGGAATGAGCC 3960
QY 3961 GTGACATTTACGCGGAGAGATATGCTTAAATTTGATCCAAATTTTCTATGAGTGT 4020
Db 3961 GTGACATTTACGCGGAGAGATATGCTTAAATTTGATCCAAATTTTCTATGAGTGT 4020
QY 4021 AATGAAGGTTATGATTTAATTTGATATGTTTCTGTTTGTATTTTACAAAGACAGAA 4080
Db 4021 AATGAAGGTTATGATTTAATTTGATATGTTTCTGTTTGTATTTTACAAAGACAGAA 4080
QY 4081 AATGTAATTTGGATTCATATGAAACAGCTGGAATTCAGAAATGTAATTAACACAGC 4140
Db 4081 AATGTAATTTGGATTCATATGAAACAGCTGGAATTCAGAAATGTAATTAACACAGC 4140
QY 4141 GCAATGGAACATGAGGACTACCTACCTAACCAAGATGTTATATATGAGATGCAAT 4200
Db 4141 GCAATGGAACATGAGGACTACCTACCTAACCAAGATGTTATATATGAGATGCAAT 4200
QY 4201 ACATTTAAATGTTATGTTGCTATATACATGCTGTTGATCAACAACATTAATGATGACAGTA 4260
Db 4201 ACATTTAAATGTTATGTTGCTATATACATGCTGTTGATCAACAACATTAATGATGACAGTA 4260
QY 4261 AACAAAGGTCGAACATCTTTCCCAAGGTTTAAATGCTGATGTAAGTCAAGTCCACA 4320
Db 4261 AACAAAGGTCGAACATCTTTCCCAAGGTTTAAATGCTGATGTAAGTCAAGTCCACA 4320

QY 4321 ATAGACAATGGGTACATAGACATTTGGCTTGCAGAGATPACAACCATGACATCAATT 4380
 |||||
 Db 4321 ATAGACAATGGGTACATAGACATTTGGCTTGCAGAGATPACAACCATGACATCAATT 4380
 QY 4381 ACTGTAAAGTGTAGCGAGCGGTACACATTTGGGGCTGAACATTAAAGTGCACAAC 4440
 |||||
 Db 4381 ACTGTAAAGTGTAGCGAGCGGTACACATTTGGGGCTGAACATTAAAGTGCACAAC 4440
 QY 4441 ACAACTTGGGTTCCACCATTTACCTAAGTGTATTAGTTACAATTAACCCAGACACCC 4500
 |||||
 Db 4441 ACAACTTGGGTTCCACCATTTACCTAAGTGTATTAGTTACAATTAACCCAGACACCC 4500
 QY 4501 ATGCGAGAAACACCCATGCGCAGAAACACCCAGCCAGATTTACAAAATTAATTTGCA 4560
 |||||
 Db 4501 ATGCGAGAAACACCCATGCGCAGAAACACCCAGCCAGATTTACAAAATTAATTTGCA 4560
 QY 4561 ACCGCTAAACTGCAACACACCAAAATGCGTTTGTACAACTGTTTCTCAGAGAAA 4620
 |||||
 Db 4561 ACCGCTAAACTGCAACACACCAAAATGCGTTTGTACAACTGTTTCTCAGAGAAA 4620
 QY 4621 GACGACGTTACTTGTGTAAACCCATTTTACGGATTCATGTTAAAGGCTGAATAAGAC 4680
 |||||
 Db 4621 GACGACGTTACTTGTGTAAACCCATTTTACGGATTCATGTTAAAGGCTGAATAAGAC 4680
 QY 4681 AAGGAAAAATACAGTGTGTGCGAGCGTTGAGCTAATATGTGACACGAGATTACTTAA 4740
 |||||
 Db 4681 AAGGAAAAATACAGTGTGTGCGAGCGTTGAGCTAATATGTGACACGAGATTACTTAA 4740
 QY 4741 ATGCACTGTACAGTTTCTGTTGAATGTTGTCCAACGGAACATGAGCTCTCAAAATGCC 4800
 |||||
 Db 4741 ATGCACTGTACAGTTTCTGTTGAATGTTGTCCAACGGAACATGAGCTCTCAAAATGCC 4800
 QY 4801 AAGTGTATAGAAAAAATGTCACAAACCCCTCAAGACCTTTAAACGGAGATTAATAATT 4860
 |||||
 Db 4801 AAGTGTATAGAAAAAATGTCACAAACCCCTCAAGACCTTTAAACGGAGATTAATAATT 4860
 QY 4861 ACAAGCGAGAAAGATGCTTTTAAAGTACGAAACAATATATATTAATGTAATGAAGAGT 4920
 |||||
 Db 4861 ACAAGCGAGAAAGATGCTTTTAAAGTACGAAACAATATATATTAATGTAATGAAGAGT 4920
 QY 4921 TATCAACTTTTAAAGATATGATGCGATTTGTATGCTTAAAGACGATTTAAAAACAGTT 4980
 |||||
 Db 4921 TATCAACTTTTAAAGATATGATGCGATTTGTATGCTTAAAGACGATTTAAAAACAGTT 4980
 QY 4981 GACTGGGAGCCAAAAGGCGCTATATGTGATTTGAAAAATGTAAGCCACGCCACAATTT 5040
 |||||
 Db 4981 GACTGGGAGCCAAAAGGCGCTATATGTGATTTGAAAAATGTAAGCCACGCCACAATTT 5040
 QY 5041 ACAAGCGAAATACATCGGCTGAAGAGCTTTATCGATTTTGGACACCGCTAAACATTT 5100
 |||||
 Db 5041 ACAAGCGAAATACATCGGCTGAAGAGCTTTATCGATTTTGGACACCGCTAAACATTT 5100
 QY 5101 TCGTGCATCGTGAATCTTTCTTAAAGTGTAGATGAATGACACGATGTAATGAATACG 5160
 |||||
 Db 5101 TCGTGCATCGTGAATCTTTCTTAAAGTGTAGATGAATGACACGATGTAATGAATACG 5160
 QY 5161 TGTGAATTAACCGTTTCCAAAGTGTGAACAATCACTTGCACGCGCTCAATATTTGCACAC 5220
 |||||
 Db 5161 TGTGAATTAACCGTTTCCAAAGTGTGAACAATCACTTGCACGCGCTCAATATTTGCACAC 5220
 QY 5221 GGAAGGCTGTAACAGGTTCTTCAAGGTTTACAAATTCGCTCAATCTGTTACCAATTTG 5280
 |||||
 Db 5221 GGAAGGCTGTAACAGGTTCTTCAAGGTTTACAAATTCGCTCAATCTGTTACCAATTTG 5280
 QY 5281 TGTGAATTAACCGTTTCTTAAAGTGTGAACAATTTTACATGCAAGATTTCAATCGTGG 5340
 |||||
 Db 5281 TGTGAATTAACCGTTTCTTAAAGTGTGAACAATTTTACATGCAAGATTTCAATCGTGG 5340
 QY 5341 GATCAGCAGCTTCTAGCTGCGTGCAGCTGTTTCAATGCTTCTGACACACCTTAACCA 5400
 |||||
 Db 5341 GATCAGCAGCTTCTAGCTGCGTGCAGCTGTTTCAATGCTTCTGACACACCTTAACCA 5400

QY 5401 GAAACCAAAAAACCAACACGCGCAGAGACACCCAAACCCAAACCCAAACAGTT 5460
 |||||
 Db 5401 GAAACCAAAAAACCAACACGCGCAGAGACACCCAAACCCAAACCCAAACAGTT 5460
 QY 5461 GGAACACATACACCATTTCAAAACACACACCAAAATCCACCAATAGACACCCCAATGAGT 5520
 |||||
 Db 5461 GGAACACATACACCATTTCAAAACACACACCAAAATCCACCAATAGACACCCCAATGAGT 5520
 QY 5521 AAATGAAAAAGGCAATGTCGTTAGTTCTTTTCCAAAGTGTGCGGCTCTTGAATTTGTA 5580
 |||||
 Db 5521 AAATGAAAAAGGCAATGTCGTTAGTTCTTTTCCAAAGTGTGCGGCTCTTGAATTTGTA 5580
 QY 5581 CTGCTGCTCTTTATTTGTTTCTTAAATACCTGTTTGTCTTACAGAGGTTGCGC 5640
 |||||
 Db 5581 CTGCTGCTCTTTATTTGTTTCTTAAATACCTGTTTGTCTTACAGAGGTTGCGC 5640
 QY 5641 AGGCAAACTGCGACGATTAACCAATCTGCCACCGCGTTGATTCGGAAATTAAGTTTA 5700
 |||||
 Db 5641 AGGCAAACTGCGACGATTAACCAATCTGCCACCGCGTTGATTCGGAAATTAAGTTTA 5700
 QY 5701 CATTTTCAAGGTTGCCAATTAAGTGGTTTAAATATTTCTATTGGTTCAATTTT 5760
 |||||
 Db 5701 CATTTTCAAGGTTGCCAATTAAGTGGTTTAAATATTTCTATTGGTTCAATTTT 5760
 QY 5761 ATGTTGACCCGTTTATAGTTATTCGCGCACCTTGTGCTACATTAATAGCAGCATCACT 5820
 |||||
 Db 5761 ATGTTGACCCGTTTATAGTTATTCGCGCACCTTGTGCTACATTAATAGCAGCATCACT 5820
 QY 5821 TTCCAGCTTATATTTTACGCTACTATGACATACGCCCTTAAGCTCACGTGGCGGAT 5880
 |||||
 Db 5821 TTCCAGCTTATATTTTACGCTACTATGACATACGCCCTTAAGCTCACGTGGCGGAT 5880
 QY 5881 TGTGGCGGGGCTGAAAAATACACAAGGGGTACATTAATCCATCCAGGGGAGACATTAAG 5940
 |||||
 Db 5881 TGTGGCGGGGCTGAAAAATACACAAGGGGTACATTAATCCATCCAGGGGAGACATTAAG 5940
 QY 5941 ACAGGTTTATTAACCTATATCGATGCGCAACAATCACGTGCTAGCAGACCTGATA 6000
 |||||
 Db 5941 ACAGGTTTATTAACCTATATCGATGCGCAACAATCACGTGCTAGCAGACCTGATA 6000
 QY 6001 GAAACACATTTTAAAGTTTGTAAAGCAATTTGAATTAACATTAATGCTTCCAAAGCA 6060
 |||||
 Db 6001 GAAACACATTTTAAAGTTTGTAAAGCAATTTGAATTAACATTAATGCTTCCAAAGCA 6060
 QY 6061 ACGCGGACAAACCCCTGGAATATATAGGGGCTCGTGGCCCAATGATGCTGCGGAT 6120
 |||||
 Db 6061 ACGCGGACAAACCCCTGGAATATATAGGGGCTCGTGGCCCAATGATGCTGCGGAT 6120
 QY 6121 ACGTGTACGCTATTCGAACAAGACTTCCCTTTGCCGAGGCGCTACTCGGCAACA 6180
 |||||
 Db 6121 ACGTGTACGCTATTCGAACAAGACTTCCCTTTGCCGAGGCGCTACTCGGCAACA 6180
 QY 6181 GACCATGTGATCTGGGCTTTCTGCGTACCAATCTTTACGACTTACAGTTGAACAG 6240
 |||||
 Db 6181 GACCATGTGATCTGGGCTTTCTGCGTACCAATCTTTACGACTTACAGTTGAACAG 6240
 QY 6241 AATTCCTCTACCGCTTAAACCCGCTTAAACCAAAAGTGAACACAGCGCTCCGCCCTTA 6300
 |||||
 Db 6241 AATTCCTCTACCGCTTAAACCCGCTTAAACCAAAAGTGAACACAGCGCTCCGCCCTTA 6300
 QY 6301 AGGTGAGTGTCTTACAGAGAGTTATTTGTTTCAAAATGCAAGTTTATTCAGGCGCG 6360
 |||||
 Db 6301 AGGTGAGTGTCTTACAGAGAGTTATTTGTTTCAAAATGCAAGTTTATTCAGGCGCG 6360
 QY 6361 TGTTTGACGTTACCGGCTTAAAGCACTATCGAGGAAGCAAGGCTCTCTTTGGGTACA 6420
 |||||
 Db 6361 TGTTTGACGTTACCGGCTTAAAGCACTATCGAGGAAGCAAGGCTCTCTTTGGGTACA 6420
 QY 6421 CGCAGTTTATAGAACCGGGCTCCACTCACACATATGGAACCCCTCTGGAATGTTCCGCGAGT 6480
 |||||
 Db 6421 CGCAGTTTATAGAACCGGGCTCCACTCACACATATGGAACCCCTCTGGAATGTTCCGCGAGT 6480
 QY 6481 TACCGACAAAGATGAGATGTTTCTTGCGCTTGTGTTTACGGAAGGTTTAAAGAAAGAC 6540

Db 6481 TACCGGCAAGATGATGATGTTCTTGCCCTTGTTGTTAGGAAAGGTTTAAGAAAGAC 6540
Qy 6541 TGTGAGAGGGCTGCTGCTCCCGGGGTGTTCCAGACCCAGAGGTGACAGATTGCCGAC 6600
Db 6541 TGTGAGAGGGCTGCTGCTCCCGGGGTGTTCCAGACCCAGAGGTGACAGATTGCCGAC 6600
Qy 6601 GCCAGCGTTTAAAGTCCGTTGACAGCAAGACCTGTTGCACTCAGCGTCTAGAA 6660
Db 6601 GCCAGCGTTTAAAGTCCGTTGACAGCAAGACCTGTTGCACTCAGCGTCTAGAA 6660
Qy 6661 TGGCAAGGTTTACCATTAAGAGGTTAGCGCGTACCTCTAGGACTCCCTTTACAGCA 6720
Db 6661 TGGCAAGGTTTACCATTAAGAGGTTAGCGCGTACCTCTAGGACTCCCTTTACAGCA 6720
Qy 6721 TCCGCCAGGCGCTGAGACTCAAGAGGTGACGCGGTCATCCAGCCACAGAAAGCAAT 6780
Db 6721 TCCGCCAGGCGCTGAGACTCAAGAGGTGACGCGGTCATCCAGCCACAGAAAGCAAT 6780
Qy 6781 TCATGCAAGACCATTAACAAAATTGCCAAGATAGTGACGCAAAAAGTTTCAACGACG 6840
Db 6841 TCCGGAAGACGAGAGCGGTGCTCCACATGATGTTGTGACAGCGTCTGCCGAGCTCG 6900
Qy 6901 CCCCTGATGAGGCTGATGTTCTGAGAGTCCCGAGAGCGGTGAGATGCTGTAAT 6960
Db 6901 CCCCTGATGAGGCTGATGTTCTGAGAGTCCCGAGAGCGGTGAGATGCTGTAAT 6960
Qy 6961 ACATAGCTGCGCCATATTTGATGTTGATGACACCAAGAGCTTAAAGCGTTAG 7020
Db 6961 ACATAGCTGCGCCATATTTGATGTTGATGACACCAAGAGCTTAAAGCGTTAG 7020
Qy 7021 AGCGGAGTGGCGCAAGCGGCTGACGTGCGGGTCAAGTTCGCTGCCAATTGCG 7080
Db 7021 AGCGGAGTGGCGCAAGCGGCTGACGTGCGGGTCAAGTTCGCTGCCAATTGCG 7080
Qy 7081 TGGCTGACCTAACTAAAGTGCAGAGCAAGCGCCAGGGGCAAAAAGGAGAGCTAAACG 7140
Db 7081 TGGCTGACCTAACTAAAGTGCAGAGCAAGCGCCAGGGGCAAAAAGGAGAGCTAAACG 7140
Qy 7141 TGTACAACTCTTTTCTCTCCAAACAGGAGTGGGGTTTAAATGAGGCCAGCATAGG 7200
Db 7141 TGTACAACTCTTTTCTCTCCAAACAGGAGTGGGGTTTAAATGAGGCCAGCATAGG 7200
Qy 7201 AAAAGGAGCGAAGGCTTAAAGGGGTACCCCTCAACGCGCTGATGGTTCTTGCTCA 7260
Db 7201 AAAAGGAGCGAAGGCTTAAAGGGGTACCCCTCAACGCGCTGATGGTTCTTGCTCA 7260
Qy 7261 CGCCGATACCTGCGCTACGCGCGCTTCTGCCCCATCTGTGGCAATGATGTT 7320
Db 7261 CGCCGATACCTGCGCTACGCGCGCTTCTGCCCCATCTGTGGCAATGATGTT 7320
Qy 7321 ATTACATGAGTCTTGTGCAACACCAAAAAGCTCCAGAAAGCGGTTTAACATGCTC 7380
Db 7321 ATTACATGAGTCTTGTGCAACACCAAAAAGCTCCAGAAAGCGGTTTAACATGCTC 7380
Qy 7381 ATTATATGCGACCGCGCAACTGAGAGTGTGACGGTATGTCAGCGGCAACGCGG 7440
Db 7381 ATTATATGCGACCGCGCAACTGAGAGTGTGACGGTATGTCAGCGGCAACGCGG 7440
Qy 7441 CAACGTGCTCAACACGCTGTTCTATAGATGAAAGATAGTTTCCGCGTAACACCC 7500
Db 7441 CAACGTGCTCAACACGCTGTTCTATAGATGAAAGATAGTTTCCGCGTAACACCC 7500
Qy 7501 CTCAGGCAAGGAGCCCTTACGTGAGTACCGGAAACCGGAGCTTTAAGACACTGAGA 7560
Db 7501 CTCAGGCAAGGAGCCCTTACGTGAGTACCGGAAACCGGAGCTTTAAGACACTGAGA 7560
Qy 7561 TTCTGGCAACTTCGAGACTTTAGAGACCGGAAGAGACGAAACCGGCGCAGAGAGC 7620
Db 7561 TTCTGGCAACTTCGAGACTTTAGAGACCGGAAGAGAGACGAAACCGGCGCAGAGAGC 7620

Db 7561 TTCTGGCAACTTCGAGACTTTAGAGACCGGAAGAGAGACGAAACCGGCGCAGAGAGC 7620
Qy 7621 ACCCAAGTACAGTACTGACAGTATGTCAGACCGGTGACAGAAAGCTATCCGATTG 7680
Db 7621 ACCCAAGTACAGTACTGACAGTATGTCAGACCGGTGACAGAAAGCTATCCGATTG 7680
Qy 7681 GAATCAACGGAAGACAGATTAATCAGTGAACCTCATCAACATCCAAAGTTTCTCA 7740
Db 7681 GAATCAACGGAAGACAGATTAATCAGTGAACCTCATCAACATCCAAAGTTTCTCA 7740
Qy 7741 GGGTGTTCAGGGTATCGACTCAATGTTGACGAGAGAGTCAAGTTCGTTAATTCGA 7800
Db 7741 GGGTGTTCAGGGTATCGACTCAATGTTGACGAGAGAGTCAAGTTCGTTAATTCGA 7800
Qy 7801 TGATTTAAATTAATCTTAATTTCCGGAGAGCTCAATGCGTCAATCAATCTCAGT 7860
Db 7801 TGATTTAAATTAATCTTAATTTCCGGAGAGCTCAATGCGTCAATCAATCTCAGT 7860
Qy 7861 TGTGTCGAACGTGATGTTGACAGCGCCGCGGTGTTCTGAAATCTGTACTACAAAT 7920
Db 7861 TGTGTCGAACGTGATGTTGACAGCGCCGCGGTGTTCTGAAATCTGTACTACAAAT 7920
Qy 7921 CCCCTGATGAGTCAATGAGATATGTCCTGCGTACTGACATGATCTAGCAAGATA 7980
Db 7921 CCCCTGATGAGTCAATGAGATATGTCCTGCGTACTGACATGATCTAGCAAGATA 7980
Qy 7981 ATCCGCGATGAGGATCTCCCTCCGAGTGGCTAAAGATGCAATTTACAGACTGTGGA 8040
Db 7981 ATCCGCGATGAGGATCTCCCTCCGAGTGGCTAAAGATGCAATTTACAGACTGTGGA 8040
Qy 8041 CGAATTTAAAGCGGCTGCTGACCGCGGGTCTCACGGGTGCGAATGAAATCG 8100
Db 8041 CGAATTTAAAGCGGCTGCTGACCGCGGGTCTCACGGGTGCGAATGAAATCG 8100
Qy 8101 TACACGGGAGCATGTTCTGACTCTTGACACCGACGCGGGTCCAAAGGTTATG 8160
Db 8101 TACACGGGAGCATGTTCTGACTCTTGACACCGACGCGGGTCCAAAGGTTATG 8160
Qy 8161 CCCCTTTAAATGACAGTTAGATGACCCGAGACCATGATGTTCTCCGAAATCAATTA 8220
Db 8161 CCCCTTTAAATGACAGTTAGATGACCCGAGACCATGATGTTCTCCGAAATCAATTA 8220
Qy 8221 AAATTAATAATTAATCAATTTTCCCAACACCGCGGATTCAGAGGGGTGCGGGGT 8280
Db 8221 AAATTAATAATTAATCAATTTTCCCAACACCGCGGATTCAGAGGGGTGCGGGGT 8280
Qy 8281 TCGTCAACCGAGGGAACAGGAGACTTACGTGTCGCGGACGCTACATGAATTC 8340
Db 8281 TCGTCAACCGAGGGAACAGGAGACTTACGTGTCGCGGACGCTACATGAATTC 8340
Qy 8341 TCAACTGCTGCATCGCGGCTGTTCCCGACACAAGACCGCGGCTGTACTGTGCG 8400
Db 8341 TCAACTGCTGCATCGCGGCTGTTCCCGACACAAGACCGCGGCTGTACTGTGCG 8400
Qy 8401 ACAAGATCTCCAGACCAACCAAAACCCAGTTCTGAAGACGTCGCGAGACGACTGG 8460
Db 8401 ACAAGATCTCCAGACCAACCAAAACCCAGTTCTGAAGACGTCGCGAGACGACTGG 8460
Qy 8461 CGGAGCTGCTGCTGCTAAAGACCAAGAGCTCCGTTCCGAGAAAGAAAGTCTGG 8520
Db 8461 CGGAGCTGCTGCTGCTAAAGACCAAGAGCTCCGTTCCGAGAAAGAAAGTCTGG 8520
Qy 8521 ACGTGTCCGATTCATCATGTCGTACGCGAGATCAAACTGAACGGGGCATTTCTAA 8580
Db 8521 ACGTGTCCGATTCATCATGTCGTACGCGAGATCAAACTGAACGGGGCATTTCTAA 8580
Qy 8581 GGGCATGTGGCCAGATTCAGTTCTACGCCACAGCTGCATGCTCACGCGGTGCTAC 8640
Db 8581 GGGCATGTGGCCAGATTCAGTTCTACGCCACAGCTGCATGCTCACGCGGTGCTAC 8640
Qy 8641 AGACGATGATGCGCGGAGATACCCGAGGTGCGGAGTCCGCGGCAATCGCACACGG 8700
Db 8641 AGACGATGATGCGCGGAGATACCCGAGGTGCGGAGTCCGCGGCAATCGCACACGG 8700

OY	8701	TGGCTACCTGGCAGAAATACGGCGGCACCGCCCTCACCGTCCAGACGACGGCGCTC	8760
Db	8701	TGGCTTACCTGGCAGAAATACGGCGGCACCGCCCTCACCGTCCAGACGACGGCGCTC	8760
OY	8761	AGCCGGTCCGCCACACAGGGCGCTGGTCCCGGTATACCGTTCCTCATGTATCTCAACA	8820
Db	8761	AGCCGGTCCGCCACAGGGCGCTGGTCCCGGTATACCGTTCCTCATGTATCTCAACA	8820
OY	8821	AATACAGGGGGGTACAGCGGAAACAACGTTTTCCACTGGCGAAACCTGGGGTACTTCG	8880
Db	8821	AATACAGGGGGGTACAGCGGAAACAACGTTTTCCACTGGCGAAACCTGGGGTACTTCG	8880
OY	8881	CGGGGGCGGGCGTGGACCGCAACTGTGGCGGAAAGCTCCCTTTAAGAAAAGGGCG	8940
Db	8881	CGGGGGCGGGCGTGGACCGCAACTGTGGCGGAAAGCTCCCTTTAAGAAAAGGGCG	8940
OY	8941	TCACGCGCATCTTAAGAAAGAGACACGTCATGATGACCCCCCATATATGACCGCTATTTA	9000
Db	8941	TCACGCGCATCTTAAGAAAGAGACACGTCATGATGACCCCCCATATATGACCGCTATTTA	9000
OY	9001	AGCAGCGCGCGGACAGACAATCAGCACGTTGAGGGCGGAAAGCGTTAAAAAGAGCGTC	9060
Db	9001	AGCAGCGCGCGGACAGACAATCAGCACGTTGAGGGCGGAAAGCGTTAAAAAGAGCGTC	9060
OY	9061	AGGGCGCTGTAGAGATTAAGACAACCTTAACCTATTGAAGTGGGTATCTTGGAGCTTA	9120
Db	9061	AGGGCGCTGTAGAGATTAAGACAACCTTAACCTATTGAAGTGGGTATCTTGGAGCTTA	9120
OY	9121	TACGACACCTGGGGAAGGGCTGCCAGGACTTAACTCCGAGAGCTGCAATATTAACTCG	9180
Db	9121	TACGACACCTGGGGAAGGGCTGCCAGGACTTAACTCCGAGAGCTGCAATATTAACTCG	9180
OY	9181	GTGACTATTGTATGTGTACGACGACAGTTTTATTAGTGTGGATTAATATGACACGTAC	9240
Db	9181	GTGACTATTGTATGTGTACGACGACAGTTTTATTAGTGTGGATTAATATGACACAGTCAG	9240
OY	9241	GCGAGCGCTGAGACTATCGAGAGACCGGGTGGCCTTAATAGAGATTCGCGAGGACGACAG	9300
Db	9241	GCGAGCGCTGAGACTATCGAGAGACCGGGTGGCCTTAATAGAGATTCGCGAGGACGACAG	9300
OY	9301	ATCTTCAGTTCGTAGACAGCAGAGATATCGCACCGCTTCTCTGTACGCCCCCGAGAAC	9360
Db	9301	ATCTTCAGTTCGTAGACAGCAGAGATATCGCACCGCTTCTCTGTACGCCCCCGAGAAC	9360
OY	9361	AGCTACGAGACCCCTAAGCGCGGGCGCCCTACTGGCGGGAAACAGAAAATTTAAACGGC	9420
Db	9361	AGCTACGAGACCCCTAAGCGCGGGCGCCCTACTGGCGGGAAACAGAAAATTTAAACGGC	9420
OY	9421	TGCTGAGAGATCTAGACCTTTAGAAAAACGCTGGACAGCGGCAACAATGGCCAGGAAAC	9480
Db	9421	TGCTGAGAGATCTAGACCTTTAGAAAAACGCTGGACAGCGGCAACAATGGCCAGGAAAC	9480
OY	9481	TTCGACGACTTTAAGCGCGAGCTGTGCGCCCTCGCGCTGACTGTAGCTTGCTTATCTTTG	9540
Db	9481	TTCGACGACTTTAAGCGCGAGCTGTGCGCCCTCGCGCTGACTGTAGCTTGCTTATCTTTG	9540
OY	9541	CGGACCCGCGAAGTATCGACGCTCCCGCATTTCTAAAAACAAAAACACAGATTAAGAAC	9600
Db	9541	CGGACCCGCGAAGTATCGACGCTCCCGCATTTCTAAAAACAAAAACACAGATTAAGAAC	9600
OY	9601	TGAACCCGGAATCTTCTGCGCTGTACGCGGCAAAACTCGGTAGAGACGTCACGCTGT	9660
Db	9601	TGAACCCGGAATCTTCTGCGCTGTACGCGGCAAAACTCGGTAGAGACGTCACGCTGT	9660
OY	9661	CGCTCGAAGTGGAGACCTTGCCCAAAAAACATCGAGCAACATCTGGCGAGCTGGAGCGCA	9720
Db	9661	CGCTCGAAGTGGAGACCTTGCCCAAAAAACATCGAGCAACATCTGGCGAGCTGGAGCGCA	9720
OY	9721	GTCCTCGGCGAGATATTGAGCCGAGAGCAATTTTGAACACTACACTGAGACCGGAAT	9780
Db	9721	GTCCTCGGCGAGATATTGAGCCGAGAGCAATTTTGAACACTACACTGAGACCGGAAT	9780

QY	9781	GTCACTATCACTACGCGTTACTTTTACGTTTACGCGGGCGGGTAAATAGATGTAAACA	9840
Db	9781	GTCACTATCACTACGCGTTACTTTTACGTTTACGCGGGCGGGTAAATAGATGTAAACA	9840
QY	9841	TGTGCGTAATTAAGATGTGAAGTGTGTGTAAAGACATAGAGAGTGTGTATATGCA	9900
Db	9841	TGTGCGTAATTAAGATGTGAAGTGTGTGTAAAGACATAGAGAGTGTGTATATGCA	9900
QY	9901	TCGGTGCAGAAAGAAAGCTGTGTCCGGATTGAAACCGGGTTCGAGCTTCTGTCAACACTGC	9960
Db	9901	TCGGTGCAGAAAGAAAGCTGTGTCCGGATTGAAACCGGGTTCGAGCTTCTGTCAACACTGC	9960
QY	9961	GGGATATCTCCCGCATCCCGACCCAGACCTATACGTACGTACGTGCTTGCCTACAGT	10020
Db	9961	GGGATATCTCCCGCATCCCGACCCAGACCTATACGTACGTACGTGCTTGCCTACAGT	10020
QY	10021	GGCTGAGGGAATGGAATCTGTACCCAAATGAGGGTTCACATTACGCGGTGTGGCAG	10080
Db	10021	GGCTGAGGGAATGGAATCTGTACCCAAATGAGGGTTCACATTACGCGGTGTGGCAG	10080
QY	10081	ACCCAGACTCGATCACCTCTGTAAAGAGTTAAGGGGAGCCAAATACAGGCGCTTTTG	10140
Db	10081	ACCCAGACTCGATCACCTCTGTAAAGAGTTAAGGGGAGCCAAATACAGGCGCTTTTG	10140
QY	10141	AGACAGAACTGAGCGACCTGGGTCTAAAGTTAAACAAACGTTTGAGCGCCACGACGACG	10200
Db	10141	AGACAGAACTGAGCGACCTGGGTCTAAAGTTAAACAAACGTTTGAGCGCCACGACGACG	10200
QY	10201	GGCTCCGGTCTCTGCAAGATCAGTTAAGGAGTCTGCTGGGGGCGATACAAAGATCACA	10260
Db	10201	GGCTCCGGTCTCTGCAAGATCAGTTAAGGAGTCTGCTGGGGGCGATACAAAGATCACA	10260
QY	10261	ATTATATTCAAACGGGTGTGCGCGTCATTCATGGAACATTCATTAATTATTTGGACG	10320
Db	10261	ATTATATTCAAACGGGTGTGCGCGTCATTCATGGAACATTCATTAATTATTTGGACG	10320
QY	10321	CCGGGCAAAACCGGCTCCAGACCGCGGACCGAAAAAGATGCTCACAAATGGCCAGACTGC	10380
Db	10321	CCGGGCAAAACCGGCTCCAGACCGCGGACCGAAAAAGATGCTCACAAATGGCCAGACTGC	10380
QY	10381	TAAACACAGAGCGCGATATGACAGAGACCGTGCCTGATTAACACCCAACTAAGGCGCA	10440
Db	10381	TAAACACAGAGCGCGATATGACAGAGACCGTGCCTGATTAACACCCAACTAAGGCGCA	10440
QY	10441	CTCACTTCTAGACTGTTTCCGACCGGATCCCATAGAAATCCCTGTCTGGGGGGGTCCTT	10500
Db	10441	CTCACTTCTAGACTGTTTCCGACCGGATCCCATAGAAATCCCTGTCTGGGGGGGTCCTT	10500
QY	10501	TTAACTCTATAGACAGACACATAAACGCACTGAGCCGGATGTCCTCCGTACGTTCTTTC	10560
Db	10501	TTAACTCTATAGACAGACACATAAACGCACTGAGCCGGATGTCCTCCGTACGTTCTTTC	10560
QY	10561	AACAGGCAAACTATACCAAGCTTATGCGAAAAACAAACGAGCTTTCACAGACTCAATA	10620
Db	10561	AACAGGCAAACTATACCAAGCTTATGCGAAAAACAAACGAGCTTTCACAGACTCAATA	10620
QY	10621	GCAATCTGCGTCAAGGGAGCGCGGATGCGAAAAACCGGACACCCCTCGAGGCCAGGA	10680
Db	10621	GCAATCTGCGTCAAGGGAGCGCGGATGCGAAAAACCGGACACCCCTCGAGGCCAGGA	10680
QY	10681	CCACACCGTGGCGGCAACCGCGGCAAGCGACGTCAATCAAGACGCAAGTATCGCAAG	10740
Db	10681	CCACACCGTGGCGGCAACCGCGGCAAGCGACGTCAATCAAGACGCAAGTATCGCAAG	10740
QY	10741	AACAGTACATGAAAAAGGTGGCCAGGGACGGCTTTAAAAAACTAACAGAGTGTCTCAGA	10800
Db	10741	AACAGTACATGAAAAAGGTGGCCAGGGACGGCTTTAAAAAACTAACAGAGTGTCTCAGA	10800
QY	10801	CGCAGAGCGCGGTGTGGCAAAAGCACTGCAATGCGCGTATGGGGGGGCGTCCGCTAG	10860
Db	10801	CGCAGAGCGCGGTGTGGCAAAAGCACTGCAATGCGCGTATGGGGGGGCGTCCGCTAG	10860
QY	10861	GCAGAGCGCTCGGACTGTGAACCACTTTTCTCTCAGAGCGGCGCTTCTGTCGCGTCCCT	10920

Db 10861 GCGAGGCGTCGAGCGTGGTGAACCATTTCTCTCAGGGGGCGCTTCGTGCGCTTCCT 10920
OY 10921 GGGAGGCGGCTGCGGCTGCGATCAGATTTTATTCGAAAACCTCAAGATCACTTAAAACT 10980
Db 10921 GGGAGGCGGCTGCGGCTGCGATCAGATTTTATTCGAAAACCTCAAGATCACTTAAAACT 10980
OY 10981 CACTATATTTCCAGCGGCTCAGTGGGAACAGCTAGAGATTATCAGCTGCACTTTACG 11040
Db 10981 CACTATATTTCCAGCGGCTCAGTGGGAACAGCTAGAGATTATCAGCTGCACTTTACG 11040
OY 11041 GCGTATTAACCGGCGGCTGAGCGGCGCAGAGGAGTCTCTTCCCGGCGCGCCAGCTGC 11100
Db 11041 GCGTATTAACCGGCGGCTGAGCGGCGCAGAGGAGTCTCTTCCCGGCGCGCCAGCTGC 11100
OY 11101 CCGTGGCCCAAGTGTTCGAGGGGGCGGGAATGCTTCGATCACAAGATGCTGTCTAG 11160
Db 11101 CCGTGGCCCAAGTGTTCGAGGGGGCGGGAATGCTTCGATCACAAGATGCTGTCTAG 11160
OY 11161 AGATGATATGCCCCCAGATTCAACCGAAGACTGATAGACACAGATTTTATCGTTTTT 11220
Db 11161 AGATGATATGCCCCCAGATTCAACCGAAGACTGATAGACACAGATTTTATCGTTTTT 11220
OY 11221 ACCAATTCGCGAAGGTGATCTCAAGCGGCTACAAAGTCCGCTGCTTTATACGAG 11280
Db 11221 ACCAATTCGCGAAGGTGATCTCAAGCGGCTACAAAGTCCGCTGCTTTATACGAG 11280
OY 11281 AGCTGCTCTCTCGGTGGGCTTTTATATGCGACGCTGGGAAAAAGAGCTGCGGATATTT 11340
Db 11281 AGCTGCTCTCTCGGTGGGCTTTTATATGCGACGCTGGGAAAAAGAGCTGCGGATATTT 11340
OY 11341 CCGTACGCGGCGAAGAACTCTCATCTCCATCTCAACCTTAAGGCTGAGCTCGGCGC 11400
Db 11341 CCGTACGCGGCGAAGAACTCTCATCTCCATCTCAACCTTAAGGCTGAGCTCGGCGC 11400
OY 11401 TGTATCTAAGCTAAGGAGAGAGCGGCGCTGCTTAATTTCTCAAAATACCGGTGGA 11460
Db 11401 TGTATCTAAGCTAAGGAGAGAGCGGCGCTGCTTAATTTCTCAAAATACCGGTGGA 11460
OY 11461 TATTTAAAGACCTGTAAGCTCTTCTGTATCATCATCTGACACTGCTCGAAGGCGCATATG 11520
Db 11461 TATTTAAAGACCTGTAAGCTCTTCTGTATCATCATCTGACACTGCTCGAAGGCGCATATG 11520
OY 11521 ATAACTAAGCGAAGCGTGTCTCTCTGCGGGGCTGGGTGTGTATTCGCGATCGGACAG 11580
Db 11521 ATAACTAAGCGAAGCGTGTCTCTCTGCGGGGCTGGGTGTGTATTCGCGATCGGACAG 11580
OY 11581 GCGGTTGGGAAACGTCACACACCCCAAGGGGCGACACCAACCGCGAAGCAACGCGG 11640
Db 11581 GCGGTTGGGAAACGTCACACACCCCAAGGGGCGACACCAACCGCGAAGCAACGCGG 11640
OY 11641 GGCCTGTGACGCCACACACCTCCGAGAACCCACCTAGGGCGAGGCGTTTAAGTTGCG 11700
Db 11641 GGCCTGTGACGCCACACACCTCCGAGAACCCACCTAGGGCGAGGCGTTTAAGTTGCG 11700
OY 11701 GTGTGAGGCGCTCGGCGCACCGGCGAATCTTCAGGTTTAACCTGGAAAAAACTGTCCG 11760
Db 11701 GTGTGAGGCGCTCGGCGCACCGGCGAATCTTCAGGTTTAACCTGGAAAAAACTGTCCG 11760
OY 11761 GGCACGAGAGACAGACGACCAAGAGAGCATCTGATGTGTAAAAAAATATTTGTC 11820
Db 11761 GGCACGAGAGAGACAGACGACCAAGAGAGCATCTGATGTGTAAAAAAATATTTGTC 11820
OY 11821 CCGCAATCTTTAAGGTGAGAGGTATCGCAAGGTGGCCACCTCGGTGACCGTATATGA 11880
Db 11821 CCGCAATCTTTAAGGTGAGAGGTATCGCAAGGTGGCCACCTCGGTGACCGTATATGA 11880
OY 11881 GGGTGGACCGAGACCGCGGTGACCGGCAAGCAAGAGGTATCCGACCGGTGCGGAGTAC 11940
Db 11881 GGGTGGACCGAGACCGCGGTGACCGGCAAGCAAGAGGTATCCGACCGGTGCGGAGTAC 11940
OY 11941 GAGATCAACCACTGAGACGAGCTACGAGTGTTCAGTGCATGCGGTAAACGTCAC 12000
Db 11941 GAGATCAACCACTGAGACGAGCTACGAGTGTTCAGTGCATGCGGTAAACGTCAC 12000

Db 11941 GAGATCAACCACTGAGACGAGCTACAGTGTTCAGTGCATGCGGTAAACGTCAC 12000
OY 12001 GGCATAGTAAACACCTACACGAGGAGACTTCACTAACAGACCGTGTTCGCAACCG 12060
Db 12001 GGCATAGTAAACACCTACACGAGGAGACTTCACTAACAGACCGTGTTCGCAACCG 12060
OY 12061 GTGAGGGGCTCAGGATTAACATCCAGCGATCTTCAGTACGCGGTGCTGTACAGACA 12120
Db 12061 GTGAGGGGCTCAGGATTAACATCCAGCGATCTTCAGTACGCGGTGCTGTACAGACA 12120
OY 12121 CCGGATGGTTCCGGGAATTTACAGGGTCAGAACACGGTCAACGCGAGTCCGAGTGGAG 12180
Db 12121 CCGGATGGTTCCGGGAATTTACAGGGTCAGAACACGGTCAACGCGAGTCCGAGTGGAG 12180
OY 12181 ATGATGCGCGTTCGGCGGAACCGTACTGTATTTTGTACCGCGCTTGGAGACAGTGA 12240
Db 12181 ATGATGCGCGTTCGGCGGAACCGTACTGTATTTTGTACCGCGCTTGGAGACAGTGA 12240
OY 12241 GAGGTCCCCCGTTCTGCGCAACAGCTCAGCTGCTGGTGGGAGAAAAACCGAAAC 12300
Db 12241 GAGGTCCCCCGTTCTGCGCAACAGCTCAGCTGCTGGTGGGAGAAAAACCGAAAC 12300
OY 12301 GGCCTGGGCGCGCGGTGCTACAAATTAACCATGTGAGACTTGGCGACCGCGACGCC 12360
Db 12301 GGCCTGGGCGCGCGGTGCTACAAATTAACCATGTGAGACTTGGCGACCGCGACGCC 12360
OY 12361 ACCACGAAACCGGGGCTTTCGCGACTGCGGAGATACACCGTATCGTGAAGCGGAG 12420
Db 12361 ACCACGAAACCGGGGCTTTCGCGACTGCGGAGATACACCGTATCGTGAAGCGGAG 12420
OY 12421 GACCCCAAGTCGGGCTGTGCGGCTGACGCTGTGAAAACTTCCCGAGGGCGATACAG 12480
Db 12421 GACCCCAAGTCGGGCTGTGCGGCTGACGCTGTGAAAACTTCCCGAGGGCGATACAG 12480
OY 12481 ACAGCGCAGAGGCGCGCTACCACTTCTGTGGCAACAGAGCTGACGCGACTTCACTGCC 12540
Db 12481 ACAGCGCAGAGGCGCGCTACCACTTCTGTGGCAACAGAGCTGACGCGACTTCACTGCC 12540
OY 12541 CCGCTCCGCAAGTAACTAATTCACGGGCGAGTACCCCTGCTCAATGATGTATTACG 12600
Db 12541 CCGCTCCGCAAGTAACTAATTCACGGGCGAGTACCCCTGCTCAATGATGTATTACG 12600
OY 12601 AAAACCTTAAGCGCACTCAAGAAAGCTGTCCGATACCCAGCAAAAGGATCGGAG 12660
Db 12601 AAAACCTTAAGCGCACTCAAGAAAGCTGTCCGATACCCAGCAAAAGGATCGGAG 12660
OY 12661 CAGTACTAGAAACGAGGGGGTCTGTTCTCTGTGACACCGCTTAACGCGGCTAACG 12720
Db 12661 CAGTACTAGAAACGAGGGGGTCTGTTCTCTGTGACACCGCTTAACGCGGCTAACG 12720
OY 12721 CTAGCTGAGAGATGCGCAATTTAAAGGCGACACGACACCCCGCACCAACCTCA 12780
Db 12721 CTAGCTGAGAGATGCGCAATTTAAAGGCGACACGACACCCCGCACCAACCTCA 12780
OY 12781 ACCGCAACCGGCTTGAAGAAAGCTGTGATAGGAACGACAGGCAACGAGCAACCTAGCG 12840
Db 12781 ACCGCAACCGGCTTGAAGAAAGCTGTGATAGGAACGACAGGCAACGAGCAACCTAGCG 12840
OY 12841 GCGCCCGACGCTCAGTTCGCTACGACAAGCTCCGCGGAGCATCAACAAGTGTGAGAG 12900
Db 12841 GCGCCCGACGCTCAGTTCGCTACGACAAGCTCCGCGGAGCATCAACAAGTGTGAGAG 12900
OY 12901 GAGCTCTCCAGGCGGTGTGCGAGAAACAGGTGAGGAGACCTACATGTGTAGCAACTG 12960
Db 12901 GAGCTCTCCAGGCGGTGTGCGAGAAACAGGTGAGGAGACCTACATGTGTAGCAACTG 12960
OY 12961 ACCAAGATTAACCCCAACAGCTAATGACGGCGATATACGGGGCGCGGTGTGCGGCAAG 13020
Db 12961 ACCAAGATTAACCCCAACAGCTAATGACGGCGATATACGGGGCGCGGTGTGCGGCAAG 13020
OY 13021 TTGTTGGGCGAGCCATCTCCGTGACGAGCTCGTGGCGGTGGACAGGCGTCCGTACAGC 13080
Db 13021 TTGTTGGGCGAGCCATCTCCGTGACGAGCTCGTGGCGGTGGACAGGCGTCCGTACAGC 13080


```
QY 13081 ATCCACAGAGCCCTCCGACGTCACCCCGGGGATGCTACTGCGGCCCGGGTACG 13140
D 13081 ATCCACAGAGCCCTCCGACGTCACCCCGGGGATGCTACTGCGGCCCGGGTACG 13140
QY 13141 TTCAGGTTCTCAACACACACGCTGTTCAAGGGCCAGCTGGAGCCAGAAAGAGATC 13200
D 13141 TTCAGGTTCTCAACACACACGCTGTTCAAGGGCCAGCTGGAGCCAGAAAGAGATC 13200
QY 13301 ATACTGACGCAACACAGGTGGAGGCGTGCAGAGAGACGTGCGAACACTACTTATAGCG 13360
D 13301 ATACTGACGCAACACAGGTGGAGGCGTGCAGAGAGACGTGCGAACACTACTTATAGCG 13360
QY 13361 AGCAAGCTAACCTACTACTCAAAAGACTAGCTCTTCGTAAGAAAAATTAACACTCCGAG 13320
D 13361 AGCAAGCTAACCTACTACTCAAAAGACTAGCTCTTCGTAAGAAAAATTAACACTCCGAG 13320
QY 13321 ATATCACCCCTCGGTACGTTCAATCGCCCTGAACCTGTCTTTATAGAAACATAGATTTC 13380
D 13321 ATATCACCCCTCGGTACGTTCAATCGCCCTGAACCTGTCTTTATAGAAACATAGATTTC 13380
QY 13381 AGGGTCAATCGAGCTGTACAGCCGCGGAGAAAAAGCTGTCCGGAGCGTTTTCGATATA 13440
D 13381 AGGGTCAATCGAGCTGTACAGCCGCGGAGAAAAAGCTGTCCGGAGCGTTTTCGATATA 13440
QY 13441 GAAACCATGTTCAAGGAATCAACTACTACTACACGACGCGCTGGCGGGGACTCCGGAGAGAC 13500
D 13441 GAAACCATGTTCAAGGAATCAACTACTACTACACGACGCGCTGGCGGGGACTCCGGAGAGAC 13500
QY 13501 CTGGACAAACAGATCGACTGAACCGGACCGCTGGCGCGGACACTGTCCGAGATAGTC 13560
D 13501 CTGGACAAACAGATCGACTGAACCGGACCGCTGGCGCGGACACTGTCCGAGATAGTC 13560
QY 13561 GCGGACCTGGGCGATGTGCGCCGACGGTGTAACTGAGCTGGCAATAGCTGATTAACCTG 13620
D 13561 GCGGACCTGGGCGATGTGCGCCGACGGTGTAACTGAGCTGGCAATAGCTGATTAACCTG 13620
QY 13621 TTCGATCAATCGTGAGCGGGGTTCACTTAATTAAGAGTCCGTTCCGGGGGATGCTC 13680
D 13621 TTCGATCAATCGTGAGCGGGGTTCACTTAATTAAGAGTCCGTTCCGGGGGATGCTC 13680
QY 13681 ATGATCTGTGATTTGGGGGCTGCTCTGATCTGTTTGGCGTAAACCGGGCGACCAAC 13740
D 13681 ATGATCTGTGATTTGGGGGCTGCTCTGATCTGTTTGGCGTAAACCGGGCGACCAAC 13740
QY 13741 GCCATGCCCGCCAGGCCCATTCAGATATCTACCCCGACATAGCAAAATGACACTCTCT 13800
D 13741 GCCATGCCCGCCAGGCCCATTCAGATATCTACCCCGACATAGCAAAATGACACTCTCT 13800
QY 13801 GGCAGTAAAGTCAGACGAGAGAGATTAATAAACAATTCGCGCGGATGACACAGCTACG 13860
D 13801 GGCAGTAAAGTCAGACGAGAGAGATTAATAAACAATTCGCGCGGATGACACAGCTACG 13860
QY 13861 CAGGAGAGCGGTAGCGGTTAGAGCAAGAGAGTACAGCGCCCTGCTTTCGGCGGC 13920
D 13861 CAGGAGAGCGGTAGCGGTTAGAGCAAGAGAGTACAGCGCCCTGCTTTCGGCGGC 13920
QY 13921 GCGTCAGACGAGCTAAACGTCGCTTAAAGGAGATTAACCGGTGAGAAAAAGAGAGCT 13980
D 13921 GCGTCAGACGAGCTAAACGTCGCTTAAAGGAGATTAACCGGTGAGAAAAAGAGAGCT 13980
QY 13981 CAAGAGTATGAATGAGCAATAACACACACGCTGACTTATTCGCGCGCGCAGAG 14040
D 13981 CAAGAGTATGAATGAGCAATAACACACACGCTGACTTATTCGCGCGCGCAGAG 14040
QY 14041 CCGGCGGCGCAATGATTCGGGCGACCGCGCGGTCCCGAGAACCTCTAGAGCGCCCGGG 14100
D 14041 CCGGCGGCGCAATGATTCGGGCGACCGCGCGGTCCCGAGAACCTCTAGAGCGCCCGGG 14100
QY 14101 CGTCCGGGCTGTATCAATCATGATTTCTTAAACCGGTACCTGGGCGCTCGGCGACCA 14160
D 14101 CGTCCGGGCTGTATCAATCATGATTTCTTAAACCGGTACCTGGGCGCTCGGCGACCA 14160
QY 14161 CGCCCCCACTACACAGAGGACCGATGCTCCGCCCTGCGCGGCGGAGCGGCTTCAG 14220
D 14161 CGCCCCCACTACACAGAGGACCGATGCTCCGCCCTGCGCGGCGGAGCGGCTTCAG 14220
QY 14221 CCGCCACACAGAGCTTTGCAAGGCTCATCCCGCTGCTTCGCAAGCCAGGGGAGCGGG 14280
D 14221 CCGCCACACAGAGCTTTGCAAGGCTCATCCCGCTGCTTCGCAAGCCAGGGGAGCGGG 14280
QY 14281 ATGATCCCGGTACAGATCCGCTTCCCGCCCAACGACTTTCGAGAAAGGTGCTCGGAGAC 14340
D 14281 ATGATCCCGGTACAGATCCGCTTCCCGCCCAACGACTTTCGAGAAAGGTGCTCGGAGAC 14340
QY 14341 GTGCTGCTGCGCAACGAAGGCTCATGTGAGCGCGCGGCGCAAGCCCGTGGCCCG 14400
D 14341 GTGCTGCTGCGCAACGAAGGCTCATGTGAGCGCGCGGCGCAAGCCCGTGGCCCG 14400
QY 14401 GACCCCAAGACCAATCCATCAGCTTTCACGCGGTACGACGCTGTGAAGAACGTAAGCG 14460
D 14401 GACCCCAAGACCAATCCATCAGCTTTCACGCGGTACGACGCTGTGAAGAACGTAAGCG 14460
QY 14461 GCGGACAGGTGTGCGGAGGTACTAGCCGCTTCCAAACGAGCATTTATCCCAAGGGAAC 14520
D 14461 GCGGACAGGTGTGCGGAGGTACTAGCCGCTTCCAAACGAGCATTTATCCCAAGGGAAC 14520
QY 14521 GTGCTCAAGCTCTGGGGCGCAACGAGAGACGACCAAGCGTGTGCAAGCTGTTCGCT 14580
D 14521 GTGCTCAAGCTCTGGGGCGCAACGAGAGACGACCAAGCGTGTGCAAGCTGTTCGCT 14580
QY 14581 CAACAGTATATTTCTACGCGAAGGTTCCACGCGGCAATTAACGTACACCAATCCTCAG 14640
D 14581 CAACAGTATATTTCTACGCGAAGGTTCCACGCGGCAATTAACGTACACCAATCCTCAG 14640
QY 14641 CAGGCCCTCAAGAACACAGCGCGCGCTGCGCGGCTTCTGACCAAGAAAGTAAAC 14700
D 14641 CAGGCCCTCAAGAACACAGCGCGCGCTGCGCGGCTTCTGACCAAGAAAGTAAAC 14700
QY 14701 AAAAGAAATTCACAAAGGTAACGAGTGGCGGAGATCCCGTCACGAGAAATACCTATAC 14760
D 14701 AAAAGAAATTCACAAAGGTAACGAGTGGCGGAGATCCCGTCACGAGAAATACCTATAC 14760
QY 14761 TCCGTTTCATGCTCTGACCTCAGGACCGCTCGCGGTGCGGGTGGAGGTTC 14820
D 14761 TCCGTTTCATGCTCTGACCTCAGGACCGCTCGCGGTGCGGGTGGAGGTTC 14820
QY 14821 GAGTCAAAAGCGTGGAGCGGCTGCGCGGTGCTTGGATCAAGGAGTTTAAACAGTGGGG 14880
D 14821 GAGTCAAAAGCGTGGAGCGGCTGCGCGGTGCTTGGATCAAGGAGTTTAAACAGTGGGG 14880
QY 14881 TGCTACTGTTGCGCGCGCGCCCGCTTGCGGCGCAAGATGCGAGAGCGGCTTG 14940
D 14881 TGCTACTGTTGCGCGCGCGCCCGCTTGCGGCGCAAGATGCGAGAGCGGCTTG 14940
QY 14941 GAGTTTGAATGCTGAGCTGGAGAGCTCAGGTTCAAGGAGACCCAGGACTGCGCCCG 15000
D 14941 GAGTTTGAATGCTGAGCTGGAGAGCTCAGGTTCAAGGAGACCCAGGACTGCGCCCG 15000
QY 15001 TACCGCAATCGGCTTGTGATGAGAGTGCATGGAAGAGGAGGATTTCCGTGGCGACG 15060
D 15001 TACCGCAATCGGCTTGTGATGAGAGTGCATGGAAGAGGAGGATTTCCGTGGCGACG 15060
QY 15061 CCGCAGCGCGAGCGGCTGATCAAGTCTCCGCTCTTCTACAGAGACCGAGAGGCGCG 15120
D 15061 CCGCAGCGCGAGCGGCTGATCAAGTCTCCGCTCTTCTACAGAGACCGAGAGGCGCG 15120
QY 15121 CCAATCCGCGCAACATAGTGTAGGCTGGGACGTGCGACCCCATCCCGGACACGAG 15180
D 15121 CCAATCCGCGCAACATAGTGTAGGCTGGGACGTGCGACCCCATCCCGGACACGAG 15180
QY 15181 GTTTGGAGTTTCGTTGGGAATGATGATGTTGTTGCTTCCGCAATGATCCGGAGC 15240
D 15181 GTTTGGAGTTTCGTTGGGAATGATGATGTTGTTGCTTCCGCAATGATCCGGAGC 15240
QY 15241 TTCGAGGTGACATTTTAAACGCGCTATTAACATCTCAAACTTGATCTCCGTACTATTC 15300
```

|||||
Db 15341 TTGAGGTGACCTTTTAAACCGCTATACATCTCAAACTTCCTCCGTACTATATC 15300
QY 15301 ACGGAGCGCTCCAGAGTGTACAACCTTCATTAAGCAATATACAAAATATAAACCGGG 15360
Db 15301 ACGGAGCGCTCCAGAGTGTACAACCTTCATTAAGCAATATACAAAATATAAACCGGG 15360
QY 15361 TCCATCTTTGAAGTTCACGAGCCCGGTGCGGGGGAGGGGGTTCATGAGGTGGTCTCA 15420
Db 15361 TCCATCTTTGAAGTTCACGAGCCCGGTGCGGGGGAGGGGGTTCATGAGGTGGTCTCA 15420
QY 15421 AAAATTAATAAGCGGACATGTCCTCCATAGACATGTACAGAGTGTGTCCGAAAAGCTC 15480
Db 15421 AAAATTAATAAGCGGACATGTCCTCCATAGACATGTACAGAGTGTGTCCGAAAAGCTC 15480
QY 15481 AGCCTCTCCGACTACAAACTGACAGCGGTGGCCAGGACGTGTCTGGGTGGAAAAAGAG 15540
Db 15481 AGCCTCTCCGACTACAAACTGACAGCGGTGGCCAGGACGTGTCTGGGTGGAAAAAGAG 15540
QY 15541 GACGTATCGTACAAAGACATTCCTCTGTGTTCCTCAGTCCGGCGGCGAGGCTAAG 15600
Db 15541 GACGTATCGTACAAAGACATTCCTCTGTGTTCCTCAGTCCGGCGGCGAGGCTAAG 15600
QY 15601 GTGGGAGGCTATGCGGATGAGTGCCTGCTGCTGTATGAGACCTCTTAAAAATGTTATG 15660
Db 15601 GTGGGAGGCTATGCGGATGAGTGCCTGCTGCTGTATGAGACCTCTTAAAAATGTTATG 15660
QY 15661 ATACAGGTGAGATTTTCGAGATAGCCAAAGCTGGCCAAAGATTGAGGCCAGAGCGCTCTG 15720
Db 15661 ATACAGGTGAGATTTTCGAGATAGCCAAAGCTGGCCAAAGATTGAGGCCAGAGCGCTCTG 15720
QY 15721 ACGGAGGCGCAACAGCTCCGCGGTCTCTCTGCTCTGTGAGGCGCGGCGAGGAGAAC 15780
Db 15721 ACGGAGGCGCAACAGCTCCGCGGTCTCTCTGCTCTGTGAGGCGCGGCGAGGAGAAC 15780
QY 15781 TTATATCTCCCGGTTCCAAAGCGCCGAGGAGACAGGGGGGTATAGGGGCGCGAGGTGATC 15840
Db 15781 TTATATCTCCCGGTTCCAAAGCGCCGAGGAGACAGGGGGGTATAGGGGCGCGAGGTGATC 15840
QY 15841 AACCCCATTCGCGGGTTTTCACGAGAGCGCGTCTGTGTGATTTTTCGACACCTGTATC 15900
Db 15841 AACCCCATTCGCGGGTTTTCACGAGAGCGCGTCTGTGTGATTTTTCGACACCTGTATC 15900
QY 15901 CCGAGCATCATCAGGCGCAACAACCTGTCTACTCCACATGATATACAGGACAGACCTG 15960
Db 15901 CCGAGCATCATCAGGCGCAACAACCTGTCTACTCCACATGATATACAGGACAGACCTG 15960
QY 15961 CACCTCAGCCCAACCTGACGCGCGAGCATACAGACGTGTGTGTGAGCGGCGGAGCG 16020
Db 15961 CACCTCAGCCCAACCTGACGCGCGAGCATACAGACGTGTGTGTGAGCGGCGGAGCG 16020
QY 16021 GTACATTTTGTAAAAAACACAAGCGGGAGTCTGTCTGTGGAAGACTGTAAACCTGTGG 16080
Db 16021 GTACATTTTGTAAAAAACACAAGCGGGAGTCTGTCTGTGGAAGACTGTGTAAACCTGTGG 16080
QY 16081 TTAGAAAACGGAAGGGCGATCCGGCGCACCTGTGCGCGCTGCGATACCCGTCGTATAAA 16140
Db 16081 TTAGAAAACGGAAGGGCGATCCGGCGCACCTGTGCGCGCTGCGATACCCGTCGTATAAA 16140
QY 16141 ACCATCTAGATTAACACAGGTGGCCATCAAGGTGACATGTAAAGCGGTTTACGGGTTTC 16200
Db 16141 ACCATCTAGATTAACACAGGTGGCCATCAAGGTGACATGTAAAGCGGTTTACGGGTTTC 16200
QY 16201 ACCGGGGTGGCCAGCGGCTCTCTCCATGCAATTAACATAGCGAAAACGCTGACGCTCCGG 16260
Db 16201 ACCGGGGTGGCCAGCGGCTCTCTCCATGCAATTAACATAGCGAAAACGCTGACGCTCCGG 16260
QY 16261 GGGCGCAGATGCTGGAGATGTCAAAAGTCTTACGTGAGGCGCTGACGAGGAAGCCTG 16320
Db 16261 GGGCGCAGATGCTGGAGATGTCAAAAGTCTTACGTGAGGCGCTGACGAGGAAGCCTG 16320
QY 16321 CGAAGCGCTCTGGGTGCGAGGTGACGCGCGCTCACGGCGCGGTTTGGCTGTCTAC 16380
Db 16321 CGAAGCGCTCTGGGTGCGAGGTGACGCGCGCTCACGGCGCGGTTTGGCTGTCTAC 16380

Db 16321 CGAAGCGCTCTGGGTGCGAGGTGACGCGCGCTCACGGCGCGGTTTGGCTGTCTAC 16380
QY 16381 GGTGAACACGACTCCCTCTTTATCGGTGCGAGCGTATTTCCGCGGAAGCGCTTCGCT 16440
Db 16381 GGTGAACACGACTCCCTCTTTATCGGTGCGAGCGTATTTCCGCGGAAGCGCTTCGCT 16440
QY 16441 TTTCTGACGATCTGGCGCGCAGGATGACTGGCGACCTGTTCGCCACCATTAAGCTTA 16500
Db 16441 TTTCTGACGATCTGGCGCGCAGGATGACTGGCGACCTGTTCGCCACCATTAAGCTTA 16500
QY 16501 GAGGCGGAAAAGAGCTTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 16560
Db 16501 GAGGCGGAAAAGAGCTTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 16560
QY 16561 CTATTGAAGCAGCAAAATGTCATGAAGGGGTTGACCTATTGCGAAAAGCGCTCTCAAG 16620
Db 16561 CTATTGAAGCAGCAAAATGTCATGAAGGGGTTGACCTATTGCGAAAAGCGCTCTCAAG 16620
QY 16621 TTTGTCAAGAGCGATGCGCGCATCTGAGACCTGTGTCTCCAGATCCGGAAGTCAAG 16680
Db 16621 TTTGTCAAGAGCGATGCGCGCATCTGAGACCTGTGTCTCCAGATCCGGAAGTCAAG 16680
QY 16681 GCTGGCGCGGCGT 16740
Db 16681 GCTGGCGCGGCGT 16740
QY 16741 GCTGGCTTTATATAAAATCTGAGAGTCTCAAGCGAGCTATCTGAGACCTCGGAAACAG 16800
Db 16741 GCTGGCTTTATATAAAATCTGAGAGTCTCAAGCGAGCTATCTGAGACCTCGGAAACAG 16800
QY 16801 GTCTGCTCCATGAGAGATTAACTTACGTTCTCCACGAGCTAGCGCGCGCTGTGCAATTAC 16860
Db 16801 GTCTGCTCCATGAGAGATTAACTTACGTTCTCCACGAGCTAGCGCGCGCTGTGCAATTAC 16860
QY 16861 AAGACCAACCACTGCGCCCAACCTGGCGGAGTACCAAAAGCTGGCGAGGAGCGAGGAG 16920
Db 16861 AAGACCAACCACTGCGCCCAACCTGGCGGAGTACCAAAAGCTGGCGAGGAGCGAGGAG 16920
QY 16921 CTGCCCCAGGTGACAGTAAATCCCTACGTTGCTGTGAGCGCGCGCGGTCCTCAAG 16980
Db 16921 CTGCCCCAGGTGACAGTAAATCCCTACGTTGCTGTGAGCGCGCGCGGTCCTCAAG 16980
QY 16981 TCGGACCTGGCGGAACACCGGATTACGTACAGACACCAATTCCTCCGCGTGCAC 17040
Db 16981 TCGGACCTGGCGGAACACCGGATTACGTACAGACACCAATTCCTCCGCGTGCAC 17040
QY 17041 CTATATTTTGACAAATGTGTGACAGCGCGGCGCAACATCTGCAAGTGTGTGTGGCAAC 17100
Db 17041 CTATATTTTGACAAATGTGTGACAGCGCGGCGCAACATCTGCAAGTGTGTGTGGCAAC 17100
QY 17101 AACGCGGACCAACGCTGGCCATCTCTTCAATTTTCTCAAGTCCCGTAAAGCTGTTC 17160
Db 17101 AACGCGGACCAACGCTGGCCATCTCTTCAATTTTCTCAAGTCCCGTAAAGCTGTTC 17160
QY 17161 TGTGTGAAGCCCAATTGGAAGACCAATTAAGAGCGCGCGCACAGGAGTCCGAGGGA 17220
Db 17161 TGTGTGAAGCCCAATTGGAAGACCAATTAAGAGCGCGCGCACAGGAGTCCGAGGGA 17220
QY 17221 GAGCTGAGCGCGGAGGAGGAGCAACAGGAGACCGCAACATGCTGGTTAAAGCACTGTC 17280
Db 17221 GAGCTGAGCGCGGAGGAGGAGCAACAGGAGACCGCAACATGCTGGTTAAAGCACTGTC 17280
QY 17281 GGTGTGCTCGGCGAGCTGGAGAGTACTTTTACCGGGGTAGATTACAGTTCTGCAACCT 17340
Db 17281 GGTGTGCTCGGCGAGCTGGAGAGTACTTTTACCGGGGTAGATTACAGTTCTGCAACCT 17340
QY 17341 CACCGCGCTGCAAAAGCTTCAAGGCGACGCGGGGCTAACGCAAGTCCGACTCCCTTCTC 17400
Db 17341 CACCGCGCTGCAAAAGCTTCAAGGCGACGCGGGGCTAACGCAAGTCCGACTCCCTTCTC 17400
QY 17401 GCTGACACGATTAATCCCAACCAATTTGCGCTTGGAGACTCGTGAAGCGCTCAAGAACT 17460
Db 17401 GCTGACACGATTAATCCCAACCAATTTGCGCTTGGAGACTCGTGAAGCGCTCAAGAACT 17460


```
|||||
Db 19621 TTGGTGTGCGCGGAAAGTGGCGAGCTCTGGCCACGAGCGGCGCCGAGAGCTG 19680
QY 19681 CCGGGCGGGGTGACAGTGAAGCAGCAAAAACTGTGATGTTGAGACCATGTACCTGTTT 19740
Db 19681 CCGGGCGGGGTGACAGTGAAGCAGCAAAAACTGTGATGTTGAGACCATGTACCTGTTT 19740
QY 19741 TCCAGCTAAATTAATAAACCCTTTGCTGATGCTCACAAAGCCCAACCGTCTC 19800
Db 19741 TCCAGCTAAATTAATAAACCCTTTGCTGATGCTCACAAAGCCCAACCGTCTC 19800
QY 19801 TCAATTCGGGGGTGGCGGCGCTGGCGAACAACAAGTGGCTAAACACCCCTCCCGC 19860
Db 19801 TCAATTCGGGGGTGGCGGCGCTGGCGAACAACAAGTGGCTAAACACCCCTCCCGC 19860
QY 19801 TCAATTCGGGGGTGGCGGCGCTGGCGAACAACAAGTGGCTAAACACCCCTCCCGC 19860
Db 19801 TCAATTCGGGGGTGGCGGCGCTGGCGAACAACAAGTGGCTAAACACCCCTCCCGC 19860
QY 19861 ACCCTGGCCACACAAAACAGTTAAAGCCCTTCGTTAGATGACGTTTATTTATTTTAA 19920
Db 19861 ACCCTGGCCACACAAAACAGTTAAAGCCCTTCGTTAGATGACGTTTATTTATTTTAA 19920
QY 19921 TTACATCATAGCTAATTTGGCGGCGCGCTCCGCAAAAACATCTGTAGATATTCAGAT 19980
Db 19921 TTACATCATAGCTAATTTGGCGGCGCGCTCCGCAAAAACATCTGTAGATATTCAGAT 19980
QY 19981 GCGAAACGGCGTGAAGAACAGTCGCGGGGGCTCTGCCCTCCCAAGCGACGCGGTTT 20040
Db 19981 GCGAAACGGCGTGAAGAACAGTCGCGGGGGCTCTGCCCTCCCAAGCGACGCGGTTT 20040
QY 20041 TTCAATTAGACTCCGCGCCACCTATCTTGTATTACGGGNAAGCTCCTCAATTAGAGATC 20100
Db 20041 TTCAATTAGACTCCGCGCCACCTATCTTGTATTACGGGNAAGCTCCTCAATTAGAGATC 20100
QY 20101 GAGGGGCGACAGACACAGGTGACCGCGGAGCCAAATGCGCGGCGTCCGCGTCCCGGG 20160
Db 20101 GAGGGGCGACAGACACAGGTGACCGCGGAGCCAAATGCGCGGCGTCCGCGTCCCGGG 20160
QY 20161 CCGGTGTCCAGAGCATCTCGTGGCGGTGAGTAACTCTGTAGAGCCGCGAGCCGCGG 20220
Db 20161 CCGGTGTCCAGAGCATCTCGTGGCGGTGAGTAACTCTGTAGAGCCGCGAGCCGCGG 20220
QY 20221 AACCATGGCGTTTATACACTCGGCGCGGAAACTGCGGCGGTGGCACTCAACGTTAGA 20280
Db 20221 AACCATGGCGTTTATACACTCGGCGCGGAAACTGCGGCGGTGGCACTCAACGTTAGA 20280
QY 20281 CATCATATATGGAATGTAACAACAGCATGATGCGCGGGTACTCACAGACCGACAGAG 20340
Db 20281 CATCATATATGGAATGTAACAACAGCATGATGCGCGGGTACTCACAGACCGACAGAG 20340
QY 20341 AGTGAATGTTGGTGGTAAAGCAAGCAGCGCTGATGTTTAAACCCCACTTCAGACAG 20400
Db 20341 AGTGAATGTTGGTGGTAAAGCAAGCAGCGCTGATGTTTAAACCCCACTTCAGACAG 20400
QY 20401 GCGCGCCCTGTGCTCTGTCAGAGAGGCGGTTGCGCGGCCCACTGGGGGAGAACGTTAAT 20460
Db 20401 GCGCGCCCTGTGCTCTGTCAGAGAGGCGGTTGCGCGGCCCACTGGGGGAGAACGTTAAT 20460
QY 20461 TCCAGAGGAGTTCGGGGGAGGCGCGCAGTGAAGGCTGCGCGCCCAACAGAGAGTAA 20520
Db 20461 TCCAGAGGAGTTCGGGGGAGGCGCGCAGTGAAGGCTGCGCGCCCAACAGAGAGTAA 20520
QY 20521 CAGAAGCAACAGACAGGAAACATGACCGGTTAAATTAATCTGCTTCAATTCGCGGCGGC 20580
Db 20521 CAGAAGCAACAGACAGGAAACATGACCGGTTAAATTAATCTGCTTCAATTCGCGGCGGC 20580
QY 20581 GCGCGGTCAAGCGCAGGTCATTTAAACACACCGCGGCCCAACCCCAACGCGGGCGG 20640
Db 20581 GCGCGGTCAAGCGCAGGTCATTTAAACACACCGCGGCCCAACCCCAACGCGGGCGG 20640
QY 20641 CCGCCCTGGAAGCGGTTCTTCCATCGAAGAAACCGCGTCACAAAAAGGCGTCTGTTT 20700
Db 20641 CCGCCCTGGAAGCGGTTCTTCCATCGAAGAAACCGCGTCACAAAAAGGCGTCTGTTT 20700
QY 20701 GAACCATTTTGTGCGCATCGGGTTGTTTTCAGATAGGAAAGCGGTGTCACAAAACA 20760
Db 20701 GAACCATTTTGTGCGCATCGGGTTGTTTTCAGATAGGAAAGCGGTGTCACAAAACA 20760

|||||
Db 20701 GAACCATTTTGTGCGCATCGGGTTGTTTTCAGATAGGAAAGCGGTGTCACAAAACA 20760
QY 20761 CCCAAGGGGGGTGTGCTCAAAACGCCATCTCATATGTTGGAGTGGGGTGTGTAC 20820
Db 20761 CCCAAGGGGGGTGTGCTCAAAACGCCATCTCATATGTTGGAGTGGGGTGTGTAC 20820
QY 20821 CCTGAGACTCAGATCCGCGCGGTAAAGTCTCTCAGACGCGCCACTTTTCTCAAAATCT 20880
Db 20821 CCTGAGACTCAGATCCGCGCGGTAAAGTCTCTCAGACGCGCCACTTTTCTCAAAATCT 20880
QY 20881 TCAGCGCGGAAAGGAGACCGGGGCTCTCCGACGATGAGAGAGAGGAGATCAAGTGGT 20940
Db 20881 TCAGCGCGGAAAGGAGACCGGGGCTCTCCGACGATGAGAGAGAGGAGATCAAGTGGT 20940
QY 20941 TGTGTTAAAGCTGTGGGCGTACCCCAAGGTTGCAACAAGTCTCCCGGGGTCAAGGCCGTA 21000
Db 20941 TGTGTTAAAGCTGTGGGCGTACCCCAAGGTTGCAACAAGTCTCCCGGGGTCAAGGCCGTA 21000
QY 21001 CGTGAGCGATCAGATACGTACAGAGGCGGTAGCTGCGATGTTAAACGGGACCCGAGGC 21060
Db 21001 CGTGAGCGATCAGATACGTACAGAGGCGGTAGCTGCGATGTTAAACGGGACCCGAGGC 21060
QY 21061 CCATGTCGGGAGCTCTGTTACAGCTGGCAGAGACGTCGCCCGAGCCACAGTAAACT 21120
Db 21061 CCATGTCGGGAGCTCTGTTACAGCTGGCAGAGACGTCGCCCGAGCCACAGTAAACT 21120
QY 21121 GACACAAAAGTGAACAGAGGAGAGCCATCCGCGAGGTCCGCGGGGTTCCAGCGGC 21180
Db 21121 GACACAAAAGTGAACAGAGGAGAGCCATCCGCGAGGTCCGCGGGGTTCCAGCGGC 21180
QY 21181 ACATTAACGATGTGGCGCATGTGTGGGCGCGCTGTATATGATTCACACAGTAAACGAGT 21240
Db 21181 ACATTAACGATGTGGCGCATGTGTGGGCGCGCTGTATATGATTCACACAGTAAACGAGT 21240
QY 21241 GGTTCACCCCTGACCCCTGTGTTGGCTGTGGGCCCTGTGATCTACGCGCCCAAAATGTC 21300
Db 21241 GGTTCACCCCTGACCCCTGTGTTGGCTGTGGGCCCTGTGATCTACGCGCCCAAAATGTC 21300
QY 21301 TCCACTGGAACCGGTACACCGGCGCCAGATGCGCCCTGCGGCGGTGCCGAAGCCCTGCG 21360
Db 21301 TCCACTGGAACCGGTACACCGGCGCCAGATGCGCCCTGCGGCGGTGCCGAAGCCCTGCG 21360
QY 21361 CCGCCAAAAGGCGGGGAGCCCGTGGCGCTCCCAATTTTAAAGCGCGGCGCGACAGTT 21420
Db 21361 CCGCCAAAAGGCGGGGAGCCCGTGGCGCTCCCAATTTTAAAGCGCGGCGCGACAGTT 21420
QY 21421 CCGTGAAGTGTGGTGAAGCCCTGATTAACACAGCAAGTCTCTCAAGACGCGCCCTCAAA 21480
Db 21421 CCGTGAAGTGTGGTGAAGCCCTGATTAACACAGCAAGTCTCTCAAGACGCGCCCTCAAA 21480
QY 21481 ACAACCTTTTGTGTTAAACAGAGGAACTGTCCTCGAGTTAATGTGGGCGCTAAAGC 21540
Db 21481 ACAACCTTTTGTGTTAAACAGAGGAACTGTCCTCGAGTTAATGTGGGCGCTAAAGC 21540
QY 21541 CGAACAGGAGCTGTGGTCCAGCGCGGCTCTCCCTGCAAGCGCGGTAAATTA 21600
Db 21541 CGAACAGGAGCTGTGGTCCAGCGCGGCTCTCCCTGCAAGCGCGGTAAATTA 21600
QY 21601 TTAATTCAGTGTGCGCAAGTACTGAGCTGCGCGTGTGCGCGGCAAGCGCGAGCGGA 21660
Db 21601 TTAATTCAGTGTGCGCAAGTACTGAGCTGCGCGTGTGCGCGGCAAGCGCGAGCGGA 21660
QY 21661 CCGCGCGGCGACCTTCGCGGTGCGGAAAAAACCCGGAAGTGTGCGCGCGCGATTCAGGCA 21720
Db 21661 CCGCGCGGCGACCTTCGCGGTGCGGAAAAAACCCGGAAGTGTGCGCGCGCGATTCAGGCA 21720
QY 21721 CGCAAAAGGATTAATTTTAAAGTGAAGTACGAGATGCAAGGACCAATCATTA 21780
Db 21721 CGCAAAAGGATTAATTTTAAAGTGAAGTACGAGATGCAAGGACCAATCATTA 21780
QY 21781 TTACAAACGAGGTGCTTTACAACTATAACCGTAAACGCGCTGAAGACGAACCTTATTTAA 21840
Db 21781 TTACAAACGAGGTGCTTTACAACTATAACCGTAAACGCGCTGAAGACGAACCTTATTTAA 21840
```

QY	22921	TAAACGGAAAAATTTCCCTCACCTAACACACGCGCCGCTAACACGCAAT	22980
Db	22921	TAAACGGAAAAATTTCCCTCACCTAACACACGCGCCGCTAACACGCAAT	22980
QY	22981	ACCTTCGAAGCCGTGTGTTTAATTAACACACAGGGGTGTAAATTCGGCGGGCCCTTGG	23040
Db	22981	ACCTTCGAAGCCGTGTGTTTAATTAACACACAGGGGTGTAAATTCGGCGGGCCCTTGG	23040
QY	23041	GCCCCGCGCTGTGGGGGTGCGGTGTCTCGTGTGGTGCATCCACCACCCTGCCTGC	23100
Db	23041	GCCCCGCGCTGTGGGGGTGCGGTGTCTCGTGTGGTGCATCCACCACCCTGCCTGC	23100
QY	23101	CGAAAAACAGGCAACAACCCCTGCGCTAGTTTTTTAAAACTTAAACCCGCAAGGGGA	23160
Db	23101	CGAAAAACAGGCAACAACCCCTGCGCTAGTTTTTTAAAACTTAAACCCGCAAGGGGA	23160
QY	23161	GAGGAGACAAGGGGTGCGGTAAATGGGCTTTAGCAGCCACGCGAGCGGGAAAAAAG	23220
Db	23161	GAGGAGACAAGGGGTGCGGTAAATGGGCTTTAGCAGCCACGCGAGCGGGAAAAAAG	23220
QY	23221	GGGCAAAACGCCGGGTTAAACACAAACAGCAACAGCGCCCAACCCATATTAACACACGA	23280
Db	23221	GGGCAAAACGCCGGGTTAAACACAAACAGCAACAGCGCCCAACCCATATTAACACACGA	23280
QY	23281	TATTCCTGTGTTCGTGGGGCCGGGGTACGGCTAACCCGCGTTGGGCGTTTGCA	23340
Db	23281	TATTCCTGTGTTCGTGGGGCCGGGGTACGGCTAACCCGCGTTGGGCGTTTGCA	23340
QY	23341	AGCACGCCGCCCTTCACCCGCGCTCCCGAGGTACCGAAGGGTCAGAAACATAGTT	23400
Db	23341	AGCACGCCGCCCTTCACCCGCGCTCCCGAGGTACCGAAGGGTCAGAAACATAGTT	23400
QY	23401	TTTCAGGTCGCGCAATCGCGCGCTGGGCAACATCTTTCGGTCCCTCGAAGACCCGGAA	23460
Db	23401	TTTCAGGTCGCGCAATCGCGCGCTGGGCAACATCTTTCGGTCCCTCGAAGACCCGGAA	23460
QY	23461	AAATCCCCCGCGCGCGGTGCTTCCGAGGGCAACCGAAGATATCCCAACAGCAACCTA	23520
Db	23461	AAATCCCCCGCGCGCGGTGCTTCCGAGGGCAACCGAAGATATCCCAACAGCAACCTA	23520
QY	23521	AAGCATCATGTGTTGGGGTTCGCGTGACGCGCGCGAGAGAGAGGCGGTGTGGCGTGG	23580
Db	23521	AAGCATCATGTGTTGGGGTTCGCGTGACGCGCGCGAGAGAGAGGCGGTGTGGCGTGG	23580
QY	23581	CGAAGATATGTGGCCGCGAGACAGGGGTTCGTATGTAGACGCGCTCGACGCGTCCACT	23640
Db	23581	CGAAGATATGTGGCCGCGAGACAGGGGTTCGTATGTAGACGCGCTCGACGCGTCCACT	23640
QY	23641	GGCAGCAAGGCCAAACACAGGGGGCGCGAGCGGGCGGACAGGTGGGGCGCGCTTCCCC	23700
Db	23641	GGCAGCAAGGCCAAACACAGGGGGCGCGAGCGGGCGGACAGGTGGGGCGCGCTTCCCC	23700
QY	23701	CACGCCCGGATTTGGCAAAATGGGGAGACGGGACGCGGTTGGACGCGGCGGACGTCAA	23760
Db	23701	CACGCCCGGATTTGGCAAAATGGGGAGACGGGACGCGGTTGGACGCGGCGGACGTCAA	23760
QY	23761	TCACGACGGAGAGACGCGAGTGTGTAGTTGTCCGTCAATACCGAGGGCCGCGCGG	23820
Db	23761	TCACGACGGAGAGAGACGCGAGTGTGTAGTTGTCCGTCAATACCGAGGGCCGCGCGG	23820
QY	23821	TTGGCGATATATGAACCGCGCGGCAATTTGGAGCGTGGCGGACCAATGGCGCGT	23880
Db	23821	TTGGCGATATATGAACCGCGCGGCAATTTGGAGCGTGGCGGACCAATGGCGCGT	23880
QY	23881	TGGGTTTGTTTACAGTCCCTATATATATATATATATATACCTTCCCTGTAAAGGAATC	23940
Db	23881	TGGGTTTGTTTACAGTCCCTATATATATATATATATATATACCTTCCCTGTAAAGGAATC	23940
QY	23941	CCAGTGTCTTAAATCTATACAGCTGGGTATATATATATAGAAATACGTAATTAATTAAT	24000
Db	23941	CCAGTGTCTTAAATCTATACAGCTGGGTATATATATATATAGAAATACGTAATTAATTAAT	24000
QY	24001	TACGTATATATTTTAAATTAATTTATATTTATATTTATTAATTAATTAATTCCTGCGCT	24060

|||||
Db 24001 TACGTTATTTAAATTTATTTATTTATTTAAATTAATTCCTCCG 24060
OY 24061 TATATTAATACATCTAGTGGAAATCTACCCAGTTTATATAAATAATATTAAT 24120
Db 24061 TATATTAATACATCTAGTGGAAATCTACCCAGTTTATATAAATAATATTAAT 24120
OY 24121 CTATATAGTGGGGGTTCTAAATATGTACAAAACAATATTTTAAATTTATTCAC 24180
Db 24121 CTATATAGTGGGGGTTCTAAATATGTACAAAACAATATTTTAAATTTATTCAC 24180
OY 24181 TAAAAATGTCCTTTTACTGTGAGTACATGTATGGAATGGGAGTGTGTATAC 24240
Db 24181 TAAAAATGTCCTTTTACTGTGAGTACATGTATGGAATGGGAGTGTGTATAC 24240
OY 24241 TATGTTTCAACACACACCTTTTGGGCGCTGTAACATATATACGGAAGCTGGC 24300
Db 24241 TATGTTTCAACACACACCTTTTGGGCGCTGTAACATATATACGGAAGCTGGC 24300
OY 24301 GTTATATGCACTGGCCGCTAACACATCCCTGACAGTTGAGTTTATGCTGCTTA 24360
Db 24301 GTTATATGCACTGGCCGCTAACACATCCCTGACAGTTTATGCTGCTTA 24360
OY 24361 TGGCTTACCTGCAATCCGGGACAGCTGATTTAGTAGCACACGATTTGGGGTTTAC 24420
Db 24361 TGGCTTACCTGCAATCCGGGACAGCTGATTTAGTAGCACACGATTTGGGGTTTAC 24420
OY 24421 CCGGTTGAATTTAGTGGTTGCAAGTGTAAAAAAGCCACGAGGCTTGGGTTTAAAGCT 24480
Db 24421 CCGGTTGAATTTAGTGGTTGCAAGTGTAAAAAAGCCACGAGGCTTGGGTTTAAAGCT 24480
OY 24481 TTTAAGGCTTGGCTTTTATTAACATGCAATTTATTTATGGAAGCTATGTAATTC 24540
Db 24481 TTTAAGGCTTGGCTTTTATTAACATGCAATTTATTTATGGAAGCTATGTAATTC 24540
OY 24541 CGCATGCTTGGCTTTTATGATTTACAAAACAAGATTTGAGCCGGAATTTGTTACTGG 24600
Db 24541 CGCATGCTTGGCTTTTATGATTTACAAAACAAGATTTGAGCCGGAATTTGTTACTGG 24600
OY 24601 TACCAAAACGGCAAGCCGCTTAACACGCGCCGCTGGGCTTTTGTCTTACGCCGC 24660
Db 24601 TACCAAAACGGCAAGCCGCTTAACACGCGCCGCTGGGCTTTTGTCTTACGCCGC 24660
OY 24661 TCGCAATACATGCAATTTTAAATTTAAATGGGGCAATGCGGCAATTTTAAAGC 24720
Db 24661 TCGCAATACATGCAATTTTAAATTTAAATGGGGCAATGCGGCAATTTTAAAGC 24720
OY 24721 CGTCAAAAATTTAAATGACATACTAACCGGCTTTAGTACCTATGGCGAATTTT 24780
Db 24721 CGTCAAAAATTTAAATGACATACTAACCGGCTTTAGTACCTATGGCGAATTTT 24780
OY 24781 AAAATTTAAAGCCGCTGGGTTTAAACACAGAGCTGCCAGCTTGTATACGTTGACATATACA 24840
Db 24781 AAAATTTAAAGCCGCTGGGTTTAAACACAGAGCTGCCAGCTTGTATACGTTGACATATACA 24840
OY 24841 GTGCGGTGATTTTATGTTAGTAAAGTATTTTAACTTGAATTTTATGTTATGTTACAC 24900
Db 24841 GTGCGGTGATTTTATGTTAGTAAAGTATTTTAACTTGAATTTTATGTTATGTTACAC 24900
OY 24901 GTGATTTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAT 24960
Db 24901 GTGATTTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAT 24960
OY 24961 TTAATGTAACATTTTAAATTTTAACTGCTTATGTTATTTTGTATTTATTTATGTAAT 25020
Db 24961 TTAATGTAACATTTTAAATTTTAACTGCTTATGTTATTTTGTATTTATTTATGTAAT 25020
OY 25021 TTTGCTTTTAAATTTGTTGGGTTGTAATTTCAAGACAGGTAAAGACCTTAACTTAAATGT 25080
Db 25021 TTTGCTTTTAAATTTGTTGGGTTGTAATTTCAAGACAGGTAAAGACCTTAACTTAAATGT 25080
OY 25081 TTGCTTTGCGGCTAGCTCTAATGTTTGGCTTGGCGCTTAAAGCTTTGGCTTGG 25140
Db 25081 TTGCTTTGCGGCTAGCTCTAATGTTTGGCTTGGCGCTTAAAGCTTTGGCTTGG 25140

|||||
Db 25081 TTGCTTTGCGGCTAGCTCTAATGTTTGGCTTGGCGCTTAAAGCTTTGGCTTGG 25140
OY 25141 CCGGCTAGCTCTAATGTTTGGCTTGGCGCTTAAAGCTTTGGCTTGGCGCTAG 25200
Db 25141 CCGGCTAGCTCTAATGTTTGGCTTGGCGCTTAAAGCTTTGGCTTGGCGCTAG 25200
OY 25201 CTGCTAATGTTTGGCTTGGCGCTTAAAGCTTTGGCTTGGCGCTTAAAGCTTTGGCTTGG 25260
Db 25201 CTGCTAATGTTTGGCTTGGCGCTTAAAGCTTTGGCTTGGCGCTTAAAGCTTTGGCTTGG 25260
OY 25261 GTTGGCTTGGCGCTTAAAGCTTTGGCTTGGCGCTTAAAGCTTTGGCTTGGCGCTTAAAG 25320
Db 25261 GTTGGCTTGGCGCTTAAAGCTTTGGCTTGGCGCTTAAAGCTTTGGCTTGGCGCTTAAAG 25320
OY 25321 TGGCGCTAGCTCTAATGTTTGGCTTGGCGCTTAAAGCTTTGGCTTGGCGCTTAAAGCTTAA 25380
Db 25321 TGGCGCTAGCTCTAATGTTTGGCTTGGCGCTTAAAGCTTTGGCTTGGCGCTTAAAGCTTAA 25380
OY 25381 GTTTAAGCACATTAATTTAAAGAGCTTTGTTGTTTATGACACCTTGTATCA 25440
Db 25381 GTTTAAGCACATTAATTTAAAGAGCTTTGTTGTTTATGACACCTTGTATCA 25440
OY 25441 AACCTGCTGATTTTATCCCAACAATAATTAATTAATTAATTAATTAATTAATTAATTAAT 25500
Db 25441 AACCTGCTGATTTTATCCCAACAATAATTAATTAATTAATTAATTAATTAATTAATTAAT 25500
OY 25501 TTTGCTTGTATTTGGGTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCG 25560
Db 25501 TTTGCTTGTATTTGGGTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCG 25560
OY 25561 GCTTCCGCTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCG 25620
Db 25561 GCTTCCGCTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCG 25620
OY 25621 CCGGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGAGG 25680
Db 25621 CCGGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGAGG 25680
OY 25681 CCGGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGAGGTCCTCC 25740
Db 25681 CCGGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGAGGTCCTCC 25740
OY 25741 CCGTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGCTTCC 25800
Db 25741 CCGTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGCTTCC 25800
OY 25801 AGGATCCCGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGAGGTC 25860
Db 25801 AGGATCCCGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGAGGTC 25860
OY 25861 GCTTCCCGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGAGGTC 25920
Db 25861 GCTTCCCGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGAGGTC 25920
OY 25921 GCTTCCCGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGAGGTC 25980
Db 25921 GCTTCCCGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGAGGTC 25980
OY 25981 CCGGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGAGGTCCTCC 26040
Db 25981 CCGGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGAGGTCCTCC 26040
OY 26041 CCGTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGAGGTC 26100
Db 26041 CCGTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGAGGTC 26100
OY 26101 AGGATCCCGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGAGGTC 26160
Db 26101 AGGATCCCGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGAGGTC 26160
OY 26161 GCTTCCCGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGAGGTCCTCC 26220
Db 26161 GCTTCCCGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGCTTCCCGAGAGGTCCTCCGAGAGGTCCTCC 26220

Qy 26221 CCCCCAGGATCCCGGGCTCCCGTTCCCGAGAGGTCCCGGGCTCCCGTTCCCGAGGCT 26280
Db 26221 CCCCCAGGATCCCGGGCTCCCGTTCCCGAGAGGTCCCGGGCTCCCGTTCCCGAGGCT 26280
Qy 26281 CCGGGGCTCCCGTTCCCGAGAGGTCCCGGGCTCCCGTTCCCGAGAGGTCCCGGGCTCC 26340
Db 26281 CCGGGGCTCCCGTTCCCGAGAGGTCCCGGGCTCCCGTTCCCGAGAGGTCCCGGGCTCC 26340
Qy 26341 CCGTTCCCGAGAGGTCCCGGGCTCCCGTTCCCGAGAGGTCCCGGGCTCCCGTTCCCGG 26400
Db 26341 CCGTTCCCGAGAGGTCCCGGGCTCCCGTTCCCGAGAGGTCCCGGGCTCCCGTTCCCGG 26400
Qy 26401 AGGGTCCCGAGAGGTCCCGTTCCCGAGAGGTCCCGGGCTCCCGTTCCCGAGAGGTCCCGG 26460
Db 26401 AGGGTCCCGAGAGGTCCCGTTCCCGAGAGGTCCCGGGCTCCCGTTCCCGAGAGGTCCCGG 26460
Qy 26461 GCTCCCGTTCCCGAGAGGTCCCGGGCTCCCGTTCCCGAGAGGTCCCGGGCTCCCGTTCC 26520
Db 26461 GCTCCCGTTCCCGAGAGGTCCCGGGCTCCCGTTCCCGAGAGGTCCCGGGCTCCCGTTCC 26520
Qy 26521 CCGCGATTCAACGTTAAAGTGTATTATTTACAAACACAGTCTTTTGGCCGGGTTGGG 26580
Db 26521 CCGCGATTCAACGTTAAAGTGTATTATTTACAAACACAGTCTTTTGGCCGGGTTGGG 26580
Qy 26581 TTGTACATACACGGGGGTGCGCATTTGGCCCGCATGCAAAAATAACGTTGGGTTTCC 26640
Db 26581 TTGTACATACACGGGGGTGCGCATTTGGCCCGCATGCAAAAATAACGTTGGGTTTCC 26640
Qy 26641 GAAACGCGTAGGCTCTTACTGTTTCAATGAGCAGTCTTTCTGTACAGGTAGAGTGTAA 26700
Db 26641 GAAACGCGTAGGCTCTTACTGTTTCAATGAGCAGTCTTTCTGTACAGGTAGAGTGTAA 26700
Qy 26701 GTTTTGTGTAGCAATGCAACGAGTAGCTGCGCTGACCGGAAAGGAAAGCACTTTTAA 26760
Db 26701 GTTTTGTGTAGCAATGCAACGAGTAGCTGCGCTGACCGGAAAGGAAAGCACTTTTAA 26760
Qy 26761 CCGGAGTGTACCGCGGTGCGCATTTGCACTGTTTAACTGTTTAACTGTTTAACTGTTTAA 26820
Db 26761 CCGGAGTGTACCGCGGTGCGCATTTGCACTGTTTAACTGTTTAACTGTTTAACTGTTTAA 26820
Qy 26821 TACCTTAAGTGTAGGTAGCAATTTAGCGGGCTGTTTAACTGTTTAACTGTTTAACTG 26880
Db 26821 TACCTTAAGTGTAGGTAGCAATTTAGCGGGCTGTTTAACTGTTTAACTGTTTAACTG 26880
Qy 26881 GGAAGAAATGAATTTCTTGGCAGTTGAGTGTATGCTATGAGGGCATCTTCTTAA 26940
Db 26881 GGAAGAAATGAATTTCTTGGCAGTTGAGTGTATGCTATGAGGGCATCTTCTTAA 26940
Qy 26941 CTGTGGGTGCGGAGGAGGAGTACTTGCACATCCGCTGTTTAACTGTTTAACTGTTTAA 27000
Db 26941 CTGTGGGTGCGGAGGAGGAGTACTTGCACATCCGCTGTTTAACTGTTTAACTGTTTAA 27000
Qy 27001 TATCAGCGCTTCTTCAAGAGCAGCGCTGCTGCTAGCAGAGGCTCTTGGCCACACGA 27060
Db 27001 TATCAGCGCTTCTTCAAGAGCAGCGCTGCTGCTAGCAGAGGCTCTTGGCCACACGA 27060
Qy 27061 TTACCGCTCTGTGGGGGACATAACGCGATAGGCAAGGATGCTGCAATAAACAACGA 27120
Db 27061 TTACCGCTCTGTGGGGGACATAACGCGATAGGCAAGGATGCTGCAATAAACAACGA 27120
Qy 27121 CCGAGCGCAACACTGTGGGTGCGGCTTGGCGTGTGGGTGTTGGGTATGAGTGA 27180
Db 27121 CCGAGCGCAACACTGTGGGTGCGGCTTGGCGTGTGGGTGTTGGGTATGAGTGA 27180
Qy 27181 TAAAGTTAAGACGACGAGCTCTTTTAACTGTTGCGCATAGCCGTTCTACCCGTGTACGC 27240
Db 27181 TAAAGTTAAGACGACGAGCTCTTTTAACTGTTGCGCATAGCCGTTCTACCCGTGTACGC 27240
Qy 27241 GTAGAGGCGGTGAGTCTAGTGTCTGTTTCAACAGCGGCAATGAGGAGGAGCACTACGAA 27300
Db 27241 GTAGAGGCGGTGAGTCTAGTGTCTGTTTCAACAGCGGCAATGAGGAGGAGCACTACGAA 27300

Qy 27301 TTACTGCGAGCAATTAAGAGCATCGCCGCAACGAGAGACATGTTGTACGAGT 27360
Db 27301 TTACTGCGAGCAATTAAGAGCATCGCCGCAACGAGAGACATGTTGTACGAGT 27360
Qy 27361 TCGGGCTGTCTTGTGCGCTAGTGGCGCTTTTGGCATACAGCGATATAGTGTGCTTTA 27420
Db 27361 TCGGGCTGTCTTGTGCGCTAGTGGCGCTTTTGGCATACAGCGATATAGTGTGCTTTA 27420
Qy 27421 ACCGGATTTCCCGACCCCTAGCCTTAAGTAGAGCGATTTATATAGACCAATAAACA 27480
Db 27421 ACCGGATTTCCCGACCCCTAGCCTTAAGTAGAGCGATTTATATAGACCAATAAACA 27480
Qy 27481 AAACAAGCTAACGTTGATTTGTTGGAACATTTTATTTATTTAGAGAGTTCTTCGAGACA 27540
Db 27481 AAACAAGCTAACGTTGATTTGTTGGAACATTTTATTTATTTAGAGAGTTCTTCGAGACA 27540
Qy 27541 TTTTGTGTATGTGTACACGGGGGCGCGCTGTGGCTGTGCTTCCACCGGGGCGCGCGG 27600
Db 27541 TTTTGTGTATGTGTACACGGGGGCGCGCTGTGGCTGTGCTTCCACCGGGGCGCGCGG 27600
Qy 27601 ACTGCGCATTTGATGATCGAGGGGCGGCAAGGCGCAGCGGGGGGCGAGAGGCTGAA 27660
Db 27601 ACTGCGCATTTGATGATCGAGGGGCGGCAAGGCGCAGCGGGGGGCGAGAGGCTGAA 27660
Qy 27661 GAATGCGCTTGACATTACAGATTCTTGGGCGGCGGCGGCTGAGATTGCTGCGCTGCG 27720
Db 27661 GAATGCGCTTGACATTACAGATTCTTGGGCGGCGGCGGCTGAGATTGCTGCGCTGCG 27720
Qy 27721 CGAGACGGCGTGTGTGCTCGCCCGGCTGTGGGGGCGGTGTGCTTGTGCTGATGCCCT 27780
Db 27721 CGAGACGGCGTGTGTGCTCGCCCGGCTGTGGGGGCGGTGTGCTTGTGCTGATGCCCT 27780
Qy 27781 GCGGCTGTGTGATGAGGCTGTGGGGGCTGAGAGTGGGTTCGTTCCGGAATACACATGCG 27840
Db 27781 GCGGCTGTGTGATGAGGCTGTGGGGGCTGAGAGTGGGTTCGTTCCGGAATACACATGCG 27840
Qy 27841 GCTGTACGCTTAGGTACGCGCAGACAGCGGTAGCTGTGTGCGCAGAGAACTGAACGGCG 27900
Db 27841 GCTGTACGCTTAGGTACGCGCAGACAGCGGTAGCTGTGTGCGCAGAGAACTGAACGGCG 27900
Qy 27901 GTGGTGTGGGT 27960
Db 27901 GTGGTGTGGGT 27960
Qy 27961 GGTCCCTCAGATTCGCGCTGAAATGTCATATGTTTGTGACAGCGCATGAGCTCTGT 28020
Db 27961 GGTCCCTCAGATTCGCGCTGAAATGTCATATGTTTGTGACAGCGCATGAGCTCTGT 28020
Qy 28021 GTATGCGGACCTCTCGGCTGTGAAACACAGGCGCTGTGGAAGCTCCACGTCCTTTGC 28080
Db 28021 GTATGCGGACCTCTCGGCTGTGGAACACAGGCGCTGTGGAAGCTCCACGTCCTTTGC 28080
Qy 28081 GCTTCTGTGTGCGAGAGCGGTGCGGAGCGGTACGCTACGTGGAGATATGATGCTGCGG 28140
Db 28081 GCTTCTGTGTGCGAGAGCGGTGCGGAGCGGTACGCTACGTGGAGATATGATGCTGCGG 28140
Qy 28141 CATACGGAGAGGTTGGGGGCAACCGCGCATGGAAGGGAACGTTGCGCGAGCGGCG 28200
Db 28141 CATACGGAGAGGTTGGGGGCAACCGCGCATGGAAGGGAACGTTGCGCGAGCGGCG 28200
Qy 28201 GTGCGTACGATGAGGAGGCTACGCTAGCGGCGGATACACAGATGATACCGCGCTTG 28260
Db 28201 GTGCGTACGATGAGGAGGCTACGCTAGCGGCGGATACACAGATGATACCGCGCTTG 28260
Qy 28261 CCGGATTCGAGGAGGTGCGCACAACAGTACGTGCGGTGCGCTGTTGCGCATGTTATGCA 28320
Db 28261 CCGGATTCGAGGAGGTGCGCACAACAGTACGTGCGGTGCGCTGTTGCGCATGTTATGCA 28320
Qy 28321 GACTGCTGTGACCATGATGTCGAAAGGTGCTTGGGGAATGATGTTGTCCTCCGGGA 28380
Db 28321 GACTGCTGTGACCATGATGTCGAAAGGTGCTTGGGGAATGATGTTGTCCTCCGGGA 28380
Qy 28381 GGGCGCTCATGTTTCCGGGTGTGCGGCTTACCGCAAGTGTGAGCGCAGGAAACTGCGTTG 28440

Db	29461	GGCCTCGGTGCGCTGTTTAAAGGCTGTAAGGACGACTACTTTTGGCAACGAGGGGTTAAGCC	295250
Qy	29521	ACAGCGTAGCGGTGTTCCGGAAACCTTAACGAGATGGAAATATCTCTATAACTAGCA	29580
Db	29521	ACAGCGTAGCGGTGTTCCGGAAACCTTAACGAGATGGAAATATCTCTATAACTAGCA	29580
Qy	29581	GGCTCATACCATGTCGCTCTGTGGCACTGAGCTACGTTGGGCTTGGGGGACAG	29640
Db	29581	GGCTCATACCATGTCGCTCTGTGGCACTGAGCTACGTTGGGCTTGGGGGACAG	29640
Qy	29641	CTGACCAAGACCCCTGGGTGAGTGTGTCGCGCAGAGATTTTATACGTACTTAATPA	29700
Db	29641	CTGACCAAGACCCCTGGGTGAGTGTGTCGCGCAGAGATTTTATACGTACTTAATPA	29700
Qy	29701	TTTCCGGCCACATTATGCCAGGAACTCTTAGACAGGTGGGAACTGCCGGTAGC	29760
Db	29701	TTTCCGGCCACATTATGCCAGGAACTCTTAGACAGGTGGGAACTGCCGGGTAGC	29760
Qy	29761	GTGGCTTCGTGACAGCAGTGTGTGCGAGATTTGCGCGGTACACGGATTTCCGGGGTGG	29820
Db	29761	GTGGCTTCGTGACAGCAGTGTGTGCGAGATTTGCGCGGTACACGGATTTCCGGGGTGG	29820
Qy	29821	ATTTTGGCTCGCGGGCTCCGGCCTTAAACGTCTCAACAGACGCACTCTTTGGCTTCA	29880
Db	29821	ATTTTGGCTCGCGGGCTCCGGCCTTAAACGTCTCAACAGACGCACTCTTTGGCTTCA	29880
Qy	29881	ATAACACGCGTAGTGTAGGGTGCCTCACTACGACGTGGCGACCCGACAGTATCCAG	29940
Db	29881	ATAACACGCGTAGTGTAGGGTGCCTCACTACGACGTGGCGACCCGACAGTATCCAG	29940
Qy	29941	GACCAAAAAATAAAGCTGTGCTGATGTCGTGTAACCTCCGAAATTTGGCTTTTATATATC	30000
Db	29941	GACCAAAAAATAAAGCTGTGCTGATGTCGTGTAACCTCCGAAATTTGGCTTTTATATATC	30000
Qy	30001	GTCGTGCCAGACCGGGGGGCGATGGGTGCGGAAGATGGCGGCGACCTTCCCGGGCGT	30060
Db	30001	GTCGTGCCAGACCGGGGGGCGATGGGTGCGGAAGATGGCGGCGACCTTCCCGGGCGT	30060
Qy	30061	TAAACGTAGGAGCTTTTGAAGCTGAATCAGGCTGCCAGCGCTCCGAAACGTAGCTTTTG	30120
Db	30061	TAAACGTAGGAGCTTTTGAAGCTGAATCAGGCTGCCAGCGCTCCGAAACGTAGCTTTTG	30120
Qy	30121	GTTACAGATGTCAAAGATTTTCGTTAAATCTGGAACCGGTACAGTTTACCAAGGACGAT	30180
Db	30121	GTTACAGATGTCAAAGATTTTCGTTAAATCTGGAACCGGTACAGTTTACCAAGGACGAT	30180
Qy	30181	GTCGTTTATAGATGGATATGGCCTTTGGCCTCCACGCGCTAGATACGACCCGGGAACA	30240
Db	30181	GTCGTTTATAGATGGATATGGCCTTTGGCCTCCACGCGCTAGATACGACCCGGGAACA	30240
Qy	30241	AAACGACGTGGGGGCGCTGTGGCGCGCGCAAGAAATTTGGGAGATGTAATTTCTGTGAC	30300
Db	30241	AAACGACGTGGGGGCGCTGTGGCGCGCGCAAGAAATTTGGGAGATGTAATTTCTGTGAC	30300
Qy	30301	GAAATCAAAAAGTTGTCCCTTTTAAAGATATGTTTGGACCCGGGACGGGCTTTTACACTT	30360
Db	30301	GAAATCAAAAAGTTGTCCCTTTTAAAGATATGTTTGGACCCGGGACGGGCTTTTACACTT	30360
Qy	30361	GGAATAATCTCCACCCAGGAGCGAGGCGAGGCTTGAAGCGCCGGTGGGGGCGATCTGGGTGT	30420
Db	30361	GGAATAATCTCCACCCAGGAGCGAGGCGAGGCTTGAAGCGCCGGTGGGGGCGATCTGGGTGT	30420
Qy	30421	GATTGGGCCAGCTCCAAATAGCAAGTAAACCAAAACCTAAACAGCTAGTCCAGAGGCC	30480
Db	30421	GATTGGGCCAGCTCCAAATAGCAAGTAAACCAAAACCTAAACAGCTAGTCCAGAGGCC	30480
Qy	30481	GGCTCGGAGGTTCCATTGTTAGCCTTGAAGGAGGACGCTTTCGCTCAACAAAGTGT	30540
Db	30481	GGCTCGGAGGTTCCATTGTTAGCCTTGAAGGAGGACGCTTTCGCTCAACAAAGTGT	30540
Qy	30541	CGCAAGAGATGATACAGAGATCTGTGTCAAGGTGCTACCGGATACGGGGGTTCTTGGAAAC	30600
Db	30541	CGCAAGAGATGATACAGAGATCTGTGTCAAGGTGCTACCGGATACGGGGGTTCTTGGAAAC	30600

Db	32761	CTATGCGGAATATAGAAAATGCCCTTTTATCTATCTATAGAGGGGCGATCGGTGTTGGAA	32820
Qy	32821	AAACAACGCTATTGAATTCATGACTGGCATGTGCCGAGAGAAAAGCTTTAAAGCTGTC	32880
Db	32821	AAACAACGCTATTGAATTCATGACTGGCATGTGCCGAGAGAAAAGCTTTAAAGCTGTC	32880
Qy	32881	CCGAGCCCATGAAATTTTGGAGCTGTGTTATTTCAATATTCCTTTAAAGAACGCGAGCA	32940
Db	32881	CCGAGCCCATGAAATTTTGGAGCTGTGTTATTTCAATATTCCTTTAAAGAACGCGAGCA	32940
Qy	32941	TAGTTAAGCAAGGACCCACGGGAAATGATCATCTCTGCGCGTATACGGGTGTCAGA	33000
Db	32941	TAGTTAAGCAAGGACCCACGGGAAATGATCATCTCTGCGCGTATACGGGTGTCAGA	33000
Qy	33001	GCAAGTTTGCCTACCGTTTCTGTGCAGACGCCGCGCATCGGTGCAACCTGCAACCGT	33060
Db	33001	GCAAGTTTGCCTACCGTTTCTGTGCAGACGCCGCGCATCGGTGCAACCTGCAACCGT	33060
Qy	33061	GGCTGGTGGAAACGCTAGCACAAAGCCAGCAATTTGATTTTTCACAGACACCTAC	33120
Db	33061	GGCTGGTGGAAACGCTAGCACAAAGCCAGCAATTTGATTTTTCACAGACACCTAC	33120
Qy	33121	TGTCCGCAACGGTGGTTTTCGCTGCTGTCACGTAAAGTACAAAGCGTAAAGCGCGATC	33180
Db	33121	TGTCCGCAACGGTGGTTTTCGCTGCTGTCACGTAAAGTACAAAGCGTAAAGCGCGATC	33180
Qy	33181	ATCTGTTTCAAAATCTATCTCTTTCTCGGCACAGACGCGCATGTGCTGTTTGTCTAA	33240
Db	33181	ATCTGTTTCAAAATCTATCTCTTTCTCGGCACAGACGCGCATGTGCTGTTTGTCTAA	33240
Qy	33241	GGCTAAACGTTGAGAGGCGCACAGCGCATTCACAAAGTGAAGCCGCTAAGAGAGAAAAG	33300
Db	33241	GGCTAAACGTTGAGAGGCGCACAGCGCATTCACAAAGTGAAGCCGCTAAGAGAGAAAAG	33300
Qy	33301	GAATCAGCAAACTACTTGCACAGAGTACGCTGGGCGTACCATCGCGTGTCTGTACT	33360
Db	33301	GAATCAGCAAACTACTTGCACAGAGTACGCTGGGCGTACCATCGCGTGTCTGTACT	33360
Qy	33361	GGGTATGATGCAAAATCTCACACCGGAGCAAAATGTTTCAAGCTGTGTACAACTGTGT	33420
Db	33361	GGGTATGATGCAAAATCTCACACCGGAGCAAAATGTTTCAAGCTGTGTGTGTGTGT	33420
Qy	33421	CCATGAGGACATATGACATATGATTCAGATTCAGTTCATCCCTTAACCA	33480
Db	33421	CCATGAGGACATATGACATATGATTCAGATTCAGTTCATCCCTTAACCA	33480
Qy	33481	AACATCATGAACAGAGTATGATACCATGTGTGCAAGAAATGTTACTATCGTTAAAGAAC	33540
Db	33481	AACATCATGAACAGAGTATGATACCATGTGTGCAAGAAATGTTACTATCGTTAAAGAAC	33540
Qy	33541	ACGTACCTTAAATGAGAGTCTGTTTGGAGCTTTAAAGAGCTACGAAAGCTTCAAAATTT	33600
Db	33541	ACGTACCTTAAATGAGAGTCTGTTTGGAGCTTTAAAGAGCTACGAAAGCTTCAAAATTT	33600
Qy	33601	TAAATGTTGAGCAGAGAGACATAGATGATCGTGGGCGCTCGGGGAAATATTTATG	33660
Db	33601	TAAATGTTGAGCAGAGAGACATAGATGATCGTGGGCGCTCGGGGAAATATTTATG	33660
Qy	33661	GGCAGAGTATGCAATGAGGCTATTTAAACGACGAGTAACTGGCAGCTCTTGAAA	33720
Db	33661	GGCAGAGTATGCAATGAGGCTATTTAAACGACGAGTAACTGGCAGCTCTTGAAA	33720
Qy	33721	GCTACATTCAAACGCTAACCAAAATTTGAAGCAATGCGCGCTATTTAGTTTATATTTT	33780
Db	33721	GCTACATTCAAACGCTAACCAAAATTTGAAGCAATGCGCGCTATTTAGTTTATATTTT	33780
Qy	33781	TTTCTATATTAAGGTTTCTGTAAACGCAAAATTCGATGATGATGATGATGATGATGAT	33840
Db	33781	TTTCTATATTAAGGTTTCTGTAAACGCAAAATTCGATGATGATGATGATGATGATGAT	33840
Qy	33841	GAGTTGAATTTAATGAAACATTTACCAATTAATTTGAGAAACGTAAAGCAAGATTA	33900
Db	33841	GAGTTGAATTTAATGAAACATTTACCAATTAATTTGAGAAACGTAAAGCAAGATTA	33900
Db	33901	ACATCTATTTGTAATGGAAGATGCGTGTACGATGATGATGATGATGATGATGATGAT	33960
Qy	33901	ACATCTATTTGTAATGGAAGATGCGTGTACGATGATGATGATGATGATGATGATGAT	33960
Db	33961	ACTTTGGAAGAAAGAAAGTTTGTGCGATCAAGTATATGTTAATGTGATTAATGATG	34020
Qy	33961	ACTTTGGAAGAAAGAAAGTTTGTGCGATCAAGTATATGTTAATGTGATTAATGATG	34020
Db	34021	TATACATTTTGAATATCTTCAAGTACCAATGATTAACCTTACGCTGATTTTATATAC	34080
Qy	34021	TATACATTTTGAATATCTTCAAGTACCAATGATTAACCTTACGCTGATTTTATATAC	34080
Db	34081	AGTTCTTTCCAGGTTTACTGGAATTTTAAATGATATGACATGCTTTTAAACAGAGC	34140
Qy	34081	AGTTCTTTCCAGGTTTACTGGAATTTTAAATGATATGACATGCTTTTAAACAGAGC	34140
Db	34141	GTTTATTTAAGCAAAAGTGAATTTATTTACCACTCAACAACTATATGATCTTTTATAC	34200
Qy	34141	GTTTATTTAAGCAAAAGTGAATTTATTTACCACTCAACAACTATATGATCTTTTATAC	34200
Db	34201	GGGAAAAAATTAATGCAAGAAATTTCAAGATTTACTTTGATTTATCCATGTAATTAAT	34260
Qy	34201	GGGAAAAAATTAATGCAAGAAATTTCAAGATTTACTTTGATTTATCCATGTAATTAAT	34260
Db	34261	TCCGCAATTTAATACAGAAATTTGATATTTAGTATGATGATGATGATGATGATGATG	34320
Qy	34261	TCCGCAATTTAATACAGAAATTTGATATTTAGTATGATGATGATGATGATGATGATG	34320
Db	34321	AATATGCAATGTTGTGCACTGTGTTTGTGTCTCTACACATTTCCAGGCTTAAAGGC	34380
Qy	34321	AATATGCAATGTTGTGCACTGTGTTTGTGTCTCTACACATTTCCAGGCTTAAAGGC	34380
Db	34381	TATGATCTTATACGATTTATGCTGCTTAAATTAATTAATTAATTAATTAATTAATTA	34440
Qy	34381	TATGATCTTATACGATTTATGCTGCTTAAATTAATTAATTAATTAATTAATTAATTA	34440
Db	34441	GGCGGAAATCTTATATATCTGTTGATTTTGGCAATTTTACCAAAATTTTACAGAAATG	34500
Qy	34441	GGCGGAAATCTTATATATCTGTTGATTTTGGCAATTTTACCAAAATTTTACAGAAATG	34500
Db	34501	TTTGTTCAGTTATGATAGTCCGCTTATGCGATGATGATGATGATGATGATGATGATG	34560
Qy	34501	TTTGTTCAGTTATGATAGTCCGCTTATGCGATGATGATGATGATGATGATGATGATG	34560
Db	34561	GCTATTTGAAGCAAAAGGCTGCTGCAAAATCTTCAAAATGAAATGATATCTTATCTTC	34620
Qy	34561	GCTATTTGAAGCAAAAGGCTGCTGCAAAATCTTCAAAATGAAATGATATCTTATCTTC	34620
Db	34621	TTTTTTGAAGTTACTGCACTAATTTTATTTATTTAATAAATCTTCAAAAGCAGCAATTA	34680
Qy	34621	TTTTTTGAAGTTACTGCACTAATTTTATTTATTTAATAAATCTTCAAAAGCAGCAATTA	34680
Db	34681	GTTAAGCTTTGGGTGTTGTCAGGATGTTGACAGGTTTAAAGCTTATTAATGATTTTAA	34740
Qy	34681	GTTAAGCTTTGGGTGTTGTCAGGATGTTGACAGGTTTAAAGCTTATTAATGATTTTAA	34740
Db	34741	AGGCTCTGCTACCCCAACCTTTAAGTTATATGAGCTAATTTTGAAGGTTTGTCCATATTT	34800
Qy	34741	AGGCTCTGCTACCCCAACCTTTAAGTTATATGAGCTAATTTTGAAGGTTTGTCCATATTT	34800
Db	34801	GCAAGAGTCCAGGTTTAAATTTTAACTCCGCAAAATGCAATGATGATGATGATGATGAT	34860
Qy	34801	GCAAGAGTCCAGGTTTAAATTTTAACTCCGCAAAATGCAATGATGATGATGATGATGAT	34860
Db	34861	CAAGAGCTGATTTTCAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA	34920
Qy	34861	CAAGAGCTGATTTTCAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA	34920
Db	34921	ATTCTTAAACGAATTTGATATATTTATTTATTTATTTATTTATTTATTTATTTATTTAT	34980
Qy	34921	ATTCTTAAACGAATTTGATATATTTATTTATTTATTTATTTATTTATTTATTTATTTAT	34980

Db	38221	CGAAAACATGGCCTTCTAGACGCGAGGCGTTTCCGCTGGGCCCGAAGAACTGGGTATTAGG	38228
QY	38281	ATACGAGCCGTGTCGACGAGATGGCACACGCTGTTCCGCGACAGACATATGCAATTTGGAGCGC	38341
Db	38281	ATACGAGCCGTGTCGACGAGATGGCACACGCTGTTCCGCGACAGACATATGCAATTTGGAGCGC	38341
QY	38341	GAAATATTGGTACTCTGGGTGGAAACGTTAGTACTAGTTGACTTTGGCGTCACACAAAC	38401
Db	38341	GAAATATTGGTACTCTGGGTGGAAACGTTAGTACTAGTTGACTTTGGCGTCACACAAAC	38401
QY	38401	TACCTTTGACGGTTTTTTGGCCGGGATCCTTTTGTATATTTTCACCTGTAGATTACGTC	38461
Db	38401	TACCTTTGACGGTTTTTTGGCCGGGATCCTTTTGTATATTTTCACCTGTAGATTACGTC	38461
QY	38461	AAGCATTGATTTACTATGTTTGGTAGTCTATGATTAATTCGCTGCCACTTTGATGTC	38521
Db	38461	AAGCATTGATTTACTATGTTTGGTAGTCTATGATTAATTCGCTGCCACTTTGATGTC	38521
QY	38521	CTGAATTTGTTTTCTTGTAGAGGTTTTTAAAGTACGCGGATTTGATTCGATGTTGTG	38581
Db	38521	CTGAATTTGTTTTCTTGTAGAGGTTTTTAAAGTACGCGGATTTGATTCGATGTTGTG	38581
QY	38581	AATAATTCGCTTTGGACGCGATGCAGTTCGGATCGGAATCCAAATCCGAATAAACC	38641
Db	38581	AATAATTCGCTTTGGACGCGATGCAGTTCGGATCGGAATCCAAATCCGAATAAACC	38641
QY	38641	CAAAATGTTAAATTTAAATGTAATTCACATGACAGTTTGGCACAGGGGGCGGACACGAGC	38701
Db	38641	CAAAATGTTAAATTTAAATGTAATTCACATGACAGTTTGGCACAGGGGGCGGACACGAGC	38701
QY	38701	TAGCGTAGAGATTTTGAATGGCTCTAAAGTTTAAATTAATTCGATTAACACGTCGCAT	38761
Db	38701	TAGCGTAGAGATTTTGAATGGCTCTAAAGTTTAAATTAATTCGATTAACACGTCGCAT	38761
QY	38761	CAGATGTTCCGGCAGTGTGGCGCGTAAGGACAGCAAGCATTTCTCGAATTCGATATTGG	38821
Db	38761	CAGATGTTCCGGCAGTGTGGCGCGTAAGGACAGCAAGCATTTCTCGAATTCGATATTGG	38821
QY	38821	AAGGTAAACGACAGAGATTCGAAACATGCTTTGATTAATTACGCCACATATCAATTAATG	38881
Db	38821	AAGGTAAACGACAGAGATTCGAAACATGCTTTGATTAATTACGCCACATATCAATTAATG	38881
QY	38881	CGAACAGTACAGCAGCCGTAGAGATTGCTGTGCGCTTTGAACCAAAACCGTGTGGACAG	38941
Db	38881	CGAACAGTACAGCAGCCGTAGAGATTGCTGTGCGCTTTGAACCAAAACCGTGTGGACAG	38941
QY	38941	TTCTAGGTGAAACGGGTGGGTAAACAGTATGCGTGCATATTTGGAAATATATACATCC	39001
Db	38941	TTCTAGGTGAAACGGGTGGGTAAACAGTATGCGTGCATATTTGGAAATATATACATCC	39001
QY	39001	GATAGCATCATCAATTAATTAACCCGGTCCCGGCTACTCGTACCGGTCTTGGCAACGAT	39061
Db	39001	GATAGCATCATCAATTAATTAACCCGGTCCCGGCTACTCGTACCGGTCTTGGCAACGAT	39061
QY	39061	ACCACTTTGGGGGTATTAAGGAGTATCTCTCCCAATACAGAGCGCGGAGCGC	39121
Db	39061	ACCACTTTGGGGGTATTAAGGAGTATCTCTCCCAATACAGAGCGCGGAGCGC	39121
QY	39121	ACGGCAGCGGTAAAGGTGGTCTCTGTTTGCATAGGCTGTCCMAAGCCCTTAGCAGAC	39181
Db	39121	ACGGCAGCGGTAAAGGTGGTCTCTGTTTGCATAGGCTGTCCMAAGCCCTTAGCAGAC	39181
QY	39181	GTTTTTCAAGATCTCATTTATTTGGTGGCCAGGCAAAAAATTGGCCAGTTTGAGTTTAA	39241
Db	39181	GTTTTTCAAGATCTCATTTATTTGGTGGCCAGGCAAAAAATTGGCCAGTTTGAGTTTAA	39241
QY	39241	ATCGGAATTGGCGGTACGCGGCGTTGCTGTCACACGTAAGCAGACACGCGGCGAAG	39301
Db	39241	ATCGGAATTGGCGGTACGCGGCGTTGCTGTCACACGTAAGCAGACACGCGGCGAAG	39301
QY	39301	AACGAGGCGCTGCACAACGATTAATGAGGCGGCTCTGGAAGTACGACCCCTTTCATATAT	39361
Db	39301	AACGAGGCGCTGCACAACGATTAATGAGGCGGCTCTGGAAGTACGACCCCTTTCATATAT	39361

THCLTPVLOTIDAEEXPHVILGSAATAPVAYLAIEIRGTALTAVOTAROPVATGRL
RPTVTPMVYANKITGVGNNVNHCHGLGTFAGGVBRNIMPSSPRTKGVSAAMLRK
RHVMTPTIDILIKRAGQITSTFEASVSRVQALLIEDKNPLKSVLLELRHLRIG
KGCODLSEEDVQYIYLDYCMLTJEDVLTLDNIASQSPWMTIEDAGALIEDROADDIQ
FVSDDDIATASCPPEBQLPTPSAGALLAKKRRKINALLSDLD."

7636..9696
/gene="ORF07"
7636..9696
/gene="ORF07"
/codon_start=1
/product="transport protein"
/protein_id="AAFS9984.1"
/db_xref="GI:7329995"

/translation="MARELAALAOALSALVVDLSLVTFADPRISIDGRILIKTQLEN
LNRLDLELKEQSVETSLSEVEHLAKNIIEKLGELERLQRRSSREHFEHLIR
PECHYHSTVFOEGGGLIDVNNCLINDVELCKRLGSVYCIGANGLGRLVLE
LSTRLGISPIPHDLYVTVPVQCLREIELVNOGSLLAIDLADHCDLCKVRE
PIHGFETELSGGLKVTKRSDATOGHVRSSADLRESSLAIODNIIEFRVASIIE
LSNLIYWNACOTGLOGTENEGSOMARLLTHEADMEHRLALITPKLSATHFYCCFRD
PIESICGGI.FNSIDDTINALSRDCSTTFQOANYTNMKNQNELPRLANSILROGSA
GSOXPATPSEPRITTTAATIASVLIKDAQTRKQYMKKVARDEKFLTECLOTQAVL
ANALCMRWGVAIVGEASELVNHFLLRRFVALPWEARCRSDQILFENSKYIKNSLTS
ORLSREHVEIITLOFYGLITGPLTROSDFPGPANVLAQCFEAGMLPHHKMLVSM
IMPOIQPKDWIDQTFNRYQLPEGDINAQKSAACFIRELVLSVALYNRTMEKTRLF
SLAREKLSINLDVKGLTSGLYLYEQDAPLVLSQNTGWIIFKDIYALLYHHLQSLDC
HDN"

9683..12172
/gene="ORF08"
9683..12172
/gene="ORF08"
/codon_start=1
/product="ORF08"
/protein_id="AAFS9985.1"
/db_xref="GI:7329996"

/translation="MMITNTRRLRAMVYIIAIGTAVGENTTPKQATTTAKPTGP
STPTPENPRAPAEKFRVCSASATGELFEFNLEKCPGEDTKDTEGGLIMFKKNIV
PIHFKRYRKVATSVTVYKRGTEIATVAGOEIVRPVPOEIHMDTTCOSPMVNV
VNGIYVYDRDPTNOTFLOPVEGLTNDINOYFESOPVLYTTPGMGPGLRYRVYTPV
EIVDMTARSAPESYFVTALGDTVEVSPCHNDSTCSVAEKTENGSLVRLITVTV
FATRKPTERRVADSGEITVSKADBPASAVCALIMDKTTPPAIDTTHASHYFAN
DVATFTSLSEVANTGTYSCLDEVIQKLNQTIKLSLTHNTNSADQYKKEGGLF
LMLQPLTPLSLVDEMRLNGTTPAPATSTSVRSVNTNQAQDNLAAPOLOQAY
DKLRASINKVLEELSRAMCEQVADTYMWELESKINPTSWATIGRPSAKVGAIV
SYTDCVAVDOASVSIKSLRSTSGMCYSPVTPFPFNLSTILFKGOLGPRNLIITLD
NOVEACKETCEHFVIAENVYKYKQVFPKKITSEISLTGFIATNLESTIENDIRV
IELYSRAEKKLSGVPTDIEMFREYNTTORLAKLEDNDNTIDILNRSLDEIDRV
ADLGDGRTVVNAVSSVITLFGSIVSGFINFKSPGGMIMLIVIAVVLIVFALNR
TNAIAGAPIMTIPDIDMKQPSGCKVDQDEIKNIIAGMHQLOQEEERRRLDEQSRAPS
LFRRAADGKRRRGYKPLENEAOEYEMSK"

12290..15334
/gene="ORF09"
12290..15334
/gene="ORF09"
/codon_start=1
/product="polymerase"
/protein_id="AAFS9986.1"
/db_xref="GI:7329997"

/translation="KDFENPYLGPRGPRPHSHRGTDAPAPAGAVQPPDVCRLLPA
CLRTPGAGMIPVTLPEPTYEENGARGVLLANERSMTARBRKVAADPODOSTIF
HAYDVETTYAADRCALVEPSRFOTDIIPEGTVLKLGRGTSVCVNFPOOVYVA
KYPAGINTHIILOQALKNTAGRAAGCFSTRVYKRLIKTYDAEHVEITLTLSEGL
STLSDBLVACGCGEVESNDVARRVPLDGTFTFGYSCARATPRIAADARTALEED
CSMBEDSVQADSDMPRIVAFDIECTEBAGPCTRGDANVIOISCVFVTRBEAP
NPNPILFVGTCDPIPDVDFLEPSYEDMLVSEFMAIRPEVEFLVAGIYNISNDLPLR
ITRASOVYMLRNLNEYKIKTGSIFEVHEBRGGGSGFMARSVKIKIAGVPIIMYOYCR
EKLSLSDYKIDTVAROCGLKKEDEVYKDIPLPFRSGPGRAKVGSCYMDQVAVL
LKMFMHVEISLAKLQIARVRVLTDGOLRVFSGILFEAARBNMIIPEVPPBEOGG
YOGATYINPIRSGYDEPVIVVPASISYITIOAHNCTSTMHGRDLHLPNLDPEDY
EFTVLSGGVFHVKHRESLGLRLTLVLEKRRARLRLTACDPSLTKIILDKQOLA
IKVTCNAVYGTGVAAGSLPCINIAETVTLRGRTMLEMSKSYEALTEPDLTDLRLGRE
VTARHGAPRVYVGTDSLFIACDGSASAVAFCDLAAARTADLPPPIKLEAKT
FKCLLLTKRYIGVLLNDKMKMGVDLIRKTAACKVORCRAIIDLIVYHDEVAATA
RLCKRPPHAYVEBGLPAGFIKIVEVLANSYDLRNSVPIQLTFTSLSPVCDYK

TTNLPPLHAYOKLASRCEELPOVHDIRPIYFVNDAPGSLKSLDLAEHPDYVROHOI PVAV
DLYFDKLVHGAANLLOCLFGNNADTVAIILNLPYKLS"

15429..16679
/gene="ORF10"
15429..16679
/gene="ORF10"
/codon_start=1
/product="ORF10"
/protein_id="AAFS9987.1"
/db_xref="GI:7329998"

/translation="MLVNTLSVYLGDMEVTFHHRGFSVNLTRLOTFKGGHYARVL
PESLDOLHOPAPAGLVTRKELPRESDCYALALAPIDSGDADAARVABEYVDSRSP
LTVWNSGHRHTIRFCLELTKPLDLERAVITVGENGASBGPRTCTESLPFEGP
LRVSGASQTSPPSPFAVFEPTNASVACLILRLQVRFPSDDAARARISPKYVFSN
SGNVKASVHTLSPSKRCQOMEIITYAPDPMAEIYLGOGGVLPFTHGGRVLYGVA
DARKTPOGSSAARVOLIRQCGAARAGDLAVTGVAPELIVPALISCTTHL
RLNPNTPTTIRDTLVAAACAPVRLSSADADRDVLAASDGTALISINATPIVG
FPPVSAECSVSI.RDNGVHERNMH"

16688..17917
/gene="ORF11"
16688..17917
/gene="ORF11"
/codon_start=1
/product="ORF11"
/protein_id="AAFS9988.1"
/db_xref="GI:7329999"

/translation="MGTPVAFRFGEMQTSIYDNGTPRRYSLSVMAATTHDGYLTLYNR
SELCTVRSFCLPACPSIGRLVGRFRFPFAFASALTDGRTVFAFGRLNDPLDI
PAVERADRELVLVHAPCTTRVSRGLKFAVIAIVYVRPVGFLHFPQDRVIALTD

Query Match	26.98;	Score 10772;	DB 1;	Length 130733;
Best Local Similarity	99.48;	Pred. No. 0;		
Matches 15792;	Conservative	0;	Mismatches 98;	Indels 1;
gene				
CDS				
gene				
CDS				
5489	CACAAATCCACCAATAGACACCCCAATGAGTAATGAAAGCATGTCGTATGTC	5548		
3658	CACAAATCCACCAATAGACACCCCAATGAGTAATGAAAGCATGTCGTATGTC	3717		
5549	TTTTTGCAAGTGCCTGCTTATATGCTACTGCTGCCCTTATATGCTGTTCTAA	5608		
3718	TTTTTGCAAGTGCCTGCTTATATGCTACTGCTGCCCTTATATGCTGTTCTAA	3777		
5609	AATACGTTTGTGCTTCAGCAGGTGCGCAGCAACTGCGACGCAATTAACCAATCT	5668		
3778	AATACGTTTGTGCTTCAGCAGGTGCGCAGCAACTGCGACGCAATTAACCAATCT	3837		
5669	GCCACCGCGCTGATTCGGAATTAAGTTACATTATTCAGAGTTCGCCAATTAAGTGG	5728		
3838	GCCACCGCGCTGATTCGGAATTAAGTTACATTATTCAGAGTTCGCCAATTAAGTGG	3897		
5729	TTTAAATATTTCTATGTTGCTTATATGTTTATGACCGCTTATATGTTATCGGCC	5788		
3898	TTTAAATATTTCTATGTTGCTTATATGTTTATGACCGCTTATATGTTATCGGCC	3956		
5789	ACCTTGCGCTCATATATATAGACAGATCTTCCAGCTTATACCTTACCGACATGTA	5848		
3957	ACCTTGCGCTCATATATATAGACAGATCTTCCAGCTTATACCTTACCGACATGTA	4016		
5849	CITCATAGCGCTTAACGTACGTGCGCTGCGATTTGGCGGGCTAAATAACACAAGG	5908		
4017	CITCATAGCGCTTAACGTACGTGCGCTGCGATTTGGCGGGCTAAATAACACAAGG	4076		
5909	GGTACATTAATCATTCAGCGCGCACATTTAGACACGCTTATATAAATATATCGATGC	5968		
4077	GGTACATTAATCATTCAGCGCGCACATTTAGACACGCTTATATAAATATATCGATGC	4136		
5969	GCCACATCATCTGTCGTAGGACACATATAGAAAAACATTTTAACGTTGTTAGCA	6028		
4137	GCCACATCATCTGTCGTAGGACACATATAGAAAAACATTTTAACGTTGTTAGCA	4196		
6029	ACTGTGATTAACATTAATGCTTCCAAAGGCAAGCGGCAACACCCCTGGAAGATTAATCA	6088		
4197	ACTGTGATTAACATTAATGCTTCCAAAGGCAAGCGGCAACACCCCTGGAAGATTAATCA	4256		

QY	6089	GGGGCTTCGTCGCCCGATAGTGCGTGCGGATACGTGTACGGCTTATTCGAAACAAAGACTT	6148
Db	4257	GGGGTCCCGGTGCCCCGATAGGTGGTGCGGATACGTGTACCGCTATTCGAAACAAAGACTT	4316
QY	6149	TCCCTTTGCGGAGGCGCTCATTACGTCCGCAACAGACCATCTGGACTCTGGCGTTTCTCGCT	6208
Db	4317	TCCCTTTGCGGAGGCGCTCATTACGTCCGCAACAGACCATCTGGACTCTGGCGTTTCTCGCT	4376
QY	6209	ACCAATCCTTTACGGACTTTCAGTTTGAACAGATTCCTCTCTCACCGTTAAAGCGCGATA	6268
Db	4377	ACCAATCCTTTACGGACTTTCAGTTTGAACAGAGATTCCTCTCTCACCGTTAAAGCGCGATA	4436
QY	6289	CAAAAAAGTTGACACCACGACGCGTCCGCTTTAAGTGACGTGCTTTACACAGAGGTTAT	6328
Db	4437	CAAAAAAGTTGACACCACGACGCGTCCGCTTTAAGTGACGTCGCTTTACACAGAGGTTAT	4496
QY	6329	TGTGTTTCACAAATGCANCTTTATTCACGGCCGCTTTTGACGGTACCGGCTCTTAACGAACT	6388
Db	4497	TGTGTTTCACAAACGCAAGCTTATTCACGGCCGCTTTTGACGGTACCGGCTCTTAACGAACT	4556
QY	6389	ATGGGAGAAACCCAGGCGCTCTCTTTGGGTACACCCAGTTTTPAAACCGGGTCCACCTCA	6448
Db	4557	ATGGGAGAAACCCAGGCGCTCTCTTTGGGTACACCCAGTTTTPAAACCGGGTCCACCTCA	4616
QY	6449	CAGCATATGAAACCTCTGGAATGTCGCGACTTACCGGACAGAGATGATGTTTCTTGG	6508
Db	4617	CAGCATATGAAACCTCTGGAATGTCGCGACTTACCGGACAGAGATGATGATGTTTCTTGG	4676
QY	6509	CGTTGTTTTPACGGAAAGGCTTTAAGAAAGCTGTGGAGGGGGCGTCCGTTCCCGGGGT	6568
Db	4677	CGTTGTTTTPACGGAAAGGCTTTAAGAAAGCTGTGGAGGGGGCGTCCGTTCCCGGGGT	4736
QY	6569	GTTCCAGACCCAGAGGTGCAATTTGCCGAGCGCAGGCGCTTTTAAAGTGCCGTTGTACGA	6628
Db	4737	GTTCCAGACCCAGAGGTGCAATTTGCCGAGCGCAGGCGCTTTTAAAGTGCCGTTGTACGA	4796
QY	6629	CGAAGACCTGTTTGACACTCACGGTCAATAGAATGCCAAGGTTTACCATTAAGACGTTTGG	6688
Db	4797	CGAAGACCTGTTTGACACTCACGGTCAATAGAATGCCAAGGTTTACCATTAAGACGTTTGG	4856
QY	6689	CGCGTACCTTACGACCTCCCTCTTTTACAGCATGGCCAGGCGCTGTGAGACTCAAAAGAGCT	6748
Db	4857	CGCGTACCTTACGACCTCCCTCTTTTACAGCATGGCCAGGCGCTGTGAGACTCAAAAGAGCT	4916
QY	6749	GACGGCGGTTCATCCACGGCCACAGAAAAGCAATTCATGCAAGGACCATTTACAAATTTGCCAA	6808
Db	4917	GACGGCGGTTCATCCACGGCCACAGAAAAGCAATTCATGCAAGGACCATTTACAAATTTGCCAA	4976
QY	6809	GATAGTGCAGGCAAAAACGTTTTCACAGACGCTGCCAAAACGACACAGCGGTGTGCCCA	6868
Db	4977	GATAGTGCAGGCAAAAACGTTTTCACAGACGCTGCCAAAACGACACAGCGGTGTGCCCA	5036
QY	6869	CATGATTTGTGACACGCGTCTGCGCGAGACTGGCCCTTAGTTACGGCTGTATGTTTCTCGA	6928
Db	5037	CATGATTTGTGACACGCGTCTGCGCGAGACTGGCCCTTAGTTACGGCTGTATGTTTCTCGA	5096
QY	6929	GTTGCCCCAGGACGCGTGCAGATTGCTGAATACGATAGCTGGCCCATATTTTGAATGGTTG	6988
Db	5097	GTTGCCCCAGGACGCGTGCAGATTGCTGAATACGATAGCTGGCCCATATTTTGAATGGTTG	5156
QY	6989	TGACTCACCAAGGCTAGGTTAAGCGTTTACAGCGGTGTCGGCCGCAACAGCGCGCTTCA	7048
Db	5157	TGACTCACCAAGGCTAGGTTAAGCGTTTACAGCGGTGTCGGCCGCAACAGCGCGCTTCA	5216
QY	7049	CGTGCGGGGTAAACTGTTGCGTGCCAATTCGGTCTGTACTTAATTAAGTGCAAGACA	7108
Db	5217	CGTGCGGGGTAAACTGTTGCGTGCCAATTCGGTCTGTACTTAATTAAGTGCAAGACA	5276
QY	7109	AGCGCCCAAGGGAACAAAAGGAGACGTAAACGTGTACAACCTCTTTTCTCCACACAGG	7168
Db	5277	AGCGCCCAAGGGAACAAAAGGAGACGTAAACGTGTACAACCTCTTTTCTCCACACAGG	5336

QY	7169	ACTGGGGTTTAAATGAGGCCACGATCAGAGAAAAGCGACGCAACCCTTTAAGGCCT	7228
Dd	5337	ACTGGGGTTTTTAATGAGGGCCAGATCCAGAGAAAAGCGACGCAACCCTTTAAGGCCT	5396
QY	7229	ACCCGAACGCCCTCGATGGTTCTTGCGTTACGCCGATACCGTGGCGTACCGCGGCTC	7288
Dd	5337	ACCCGTAAAGCCCCCTCGATGGTTCTTGCGTTACGCCGATACCGTGGCGTACCGCGGCTC	5456
QY	7289	TTTCTCGCCCATTGTCGTGGCGAAGTTATGTTATTACATGCAGTCTTTGCAACACACA	7348
Dd	5457	TTTCTCGCCCATTGTCGTGGCGAAGTTATGTTATTACATGCAGTCTTTGCAACACACA	5516
QY	7349	AAGCTCCACGAACCAAGCGCTTTAAACATGTCATTATGTGGCACCGCGCCAACCTAGA	7408
Dd	5517	AAGCTCCACGAACCAAGCGCTTTAAACATGTCATTATGTGGCACCGCGCCAACCTAGA	5576
QY	7409	GATGGCAGCGTATGTCTACGGSCAACCGCGGCAACGTCCTCAACAGCGCTTCTATAG	7468
Dd	5577	GATGGCAGCGTATGTCTACGGSCAACCGCGGCAACGTCCTCAACAGCGCTTCTATAG	5636
QY	7469	ACTGAAGATAGTTTTCCCGCCGTAACACCCCTCAGCGGAGGGAACCCCTACGTGTAGAC	7528
Dd	5637	ACTGAAGATAGTTTTCCCGCCGTAACACCCCTCAGCGGAGGGAACCCCTACGTGTAGAC	5696
QY	7529	CGGAAACAGCGCGGACCTTTAAACGACCTGEGAGATTTCTGGGCACTTTCGAGCCTTTAGA	7588
Dd	5697	CGGAAACAGCGCGGACCTTTAAACGACCTGEGAGATTTCTGGGCACTTTCGAGCCTTTAGA	5756
QY	7589	CCGGCAACGAGACGGAAMCCGGCCGACGACACCCAAAGTACACGTACGTGGCAGTATG	7648
Dd	5757	CCGGCAACGAGACGGAAMCCGGCCGACGACACCCAAAGTACACGTACGTGGCAGTATG	5816
QY	7649	TCAGACCTGACAGAAAAAGCTATCCGCGATTGGATCACCGAACAACAGATATCACAGT	7708
Dd	5817	TCAGACCTGACAGAAAAAGCTATCCGCGATTGGATCACCGAACAACAGATATCACAGT	5876
QY	7709	GAACCTCATCACCAACATCCAAAGTTTTCTCAGGGTGTTCAAGSGTATCGACTCAATGT	7768
Dd	5877	GAACCTCATCACCAACATCCAAAGTTTTCTCAGGGTGTTCAAGSGTATCGACTCAATGT	5936
QY	7769	GGAGCGAAGAGTCAGTACGTTCTGTTAAATGATATAAATTAACCTTAAATTCGCCGA	7828
Dd	5937	GGAGCGAAGAGTCAGTACGTTCTGTTAAATGATATAAATTAACCTTAAATTCGCCGA	5996
QY	7829	GCAGTCGAAATCGGTCATCATACATACCTCAGCTGCGCAACGCTGATTGGCAGCGGCC	7888
Dd	5997	GCAGTCGAAATCGGTCATCATACATACCTCAGCTGCGCAACGCTGATTGGCAGCGGCC	6056
QY	7889	GTGCGCGGTGTTCTGTAATCTGTACTACAAATCCCTGCTGTGATCATTCAGATATCTG	7948
Dd	6057	GTGCGCGGTGTTCTGTAATCTGTACTACAAATCCCTGCTGTGATCATTCAGATATCTG	6116
QY	7949	CCTGCGGTACGATGATCTACGAACAAGATTAATCCGGCGATGGGCAATCCCTCCCTCCGA	8008
Dd	6117	CCTGCGGTACGATGATCTACGAACAAGATTAATCCGGCGATGGGCAATCCCTCCCTCCGA	6176
QY	8009	GTGGCTAAGATGCAATTTTCAGAGGTTGTGACGAACCTTTAAACCGGGGTTCTCGACCG	8068
Dd	6177	GTGGCTAAGATGCAATTTTCAGAGGTTGTGACGAACCTTTAAACCGGGGTTCTCGACCG	6236
QY	8069	CGGGGTCTCAGGGGGTGCGAACGTGAANAATGTAACCGGGACATGTTTTCGCACTTCT	8128
Dd	6237	CGGGGTCTCAGGGGGTGCGAACGTGAANAATGTAACCGGGACATGTTTTCGCACTTCT	6296
QY	8129	CGACACCGACGGGGGTCCACAGGCTTAATGGCCCCCTTTAAATGCAAGTTAATAATAGC	8188
Dd	6297	CGACACCGACGGGGGTCCACAGGCTTAATGGCCCCCTTTAAATGCAAGTTAATAATAGC	6356
QY	8189	CCGAGCCATGATGGTCGTTTCGGAATCAATTAATAATAAAAATGAATCATTTTTCGCA	8248
Dd	6357	CCGAGCCATGATGGTCGTTTCGGAATCAATTAATAATAAAAATGAATCATTTTTCGCA	6416
QY	8249	CACCCCGGATCCGAGGGCGTACGATCGGGGTTGCTCAACCGACGGGAACGAGGACAC	8308

|||||
Db 6417 CACCGCGGATTCGAGCGGTGCAAGTGGGGTGTGTAACCGACGGGAACCGAGGACAC 6476
OY 8309 TTACGTGTGGCGGACCGTACATGAGATTCTCACTCGCTCATGGCCGCTGTCC 8368
Db 6477 TTACGTGTGGCGGACCGTACATGAGATTCTCACTCGCTCATGGCCGCTGTCC 6536
OY 8369 CGACACCAAGACCGCGCGCTGTACTGTGTGGCAACAGATCTCCACACCAACAAACCC 8428
Db 6537 CGACACCAAGACCGCGCGCTGTACTGTGTGGCAACAGATCTCCACACCAACAAACCC 6596
OY 8429 AGTTCTGAAGACGTCCCGAGACGAGTGGGGAGCTGTGTGACGTAAAGACCA 8488
Db 6597 AGTTCTGAAGACGTCCCGAGACGAGTGGGGAGCTGTGTGACGTAAAGACCA 6656
OY 8489 CACCTGTGCTGAGAGAAAGCAAGCTGTGAGAGTGTTCGGATTCACTCATGTCTGA 8548
Db 6657 CACCTGTGCTGAGAGAAAGCAAGCTGTGAGAGTGTTCGGATTCACTCATGTCTGA 6716
OY 8549 CGGAGAGATCAAACTGAACGGGGCATTTCTAAGGCAATGTGGCCAGATTCTAAGCC 8608
Db 6717 CGGAGAGATCAAACTGAACGGGGCATTTCTAAGGCAATGTGGCCAGATTCTAAGCC 6776
OY 8609 CAGAGCTGTGCTGCTCAGCGCGGTCTACAGAGATGATCGAGGAAATACCCCA 8668
Db 6777 CAGAGCTGTGCTGCTCAGCGCGGTCTACAGAGATGATCGAGGAAATACCCCA 6836
OY 8669 CGTGTGGGCTCGCGGCAATCGCACACCGGTGCTTACCTGTGGCAAAATACGCGCG 8728
Db 6837 CGTGTGGGCTCGCGGCAATCGCACACCGGTGCTTACCTGTGGCAAAATACGCGCG 6896
OY 8729 CACCGGCTTCACCGTCCACAGACGCGCGGTGACGCGGTGCGCCACAGCGCGCTGCG 8788
Db 6897 CACCGGCTTCACCGTCCACAGACGCGCGGTGACGCGGTGCGCCACAGCGCGCTGCG 6956
OY 8789 TCCCGTATACCGTTCCTCATGTGTAGTCAACAATACAGGGGTCAAGGGAAACAAC 8848
Db 6957 TCCCGTATACCGTTCCTCATGTGTAGTCAACAATACAGGGGTCAAGGGAAACAAC 7016
OY 8849 CGTTTTCACTGCGGAAACCTGGGTACTTCCGCGGGCGGGGTGAGACCGCAACTGTG 8908
Db 7017 CGTTTTCACTGCGGAAACCTGGGTACTTCCGCGGGCGGGGTGAGACCGCAACTGTG 7076
OY 8909 GCGGAAAGCTCCCCCTTTAAGAAACGGGCGTACGCGCATCTAAGAAAGACACGT 8968
Db 7077 GCGGAAAGCTCCCCCTTTAAGAAACGGGCGTACGCGCATCTAAGAAAGACACGT 7136
OY 8969 CATGATGACCCCATTTATGACGCGCTAATAAAGCAGCGCGGAGACACATCGAC 9028
Db 7137 CATGATGACCCCATTTATGACGCGCTAATAAAGCAGCGCGGAGACACATCGAC 7196
OY 9029 GTTCGAGCGGAAAGCGTTAAAGAGCGTGCAGCGGTGTTAGAGATTAAGACAACC 9088
Db 7197 GTTCGAGCGGAAAGCGTTAAAGAGCGTGCAGCGGTGTTAGAGATTAAGACAACC 7256
OY 9089 TAACCATTAAGATGGGTATCTGTGAGGTATATAGACACCTGGGAAAGGCTGCCAGA 9148
Db 7257 TAACCATTAAGATGGGTATCTGTGAGGTATATAGACACCTGGGAAAGGCTGCCAGA 7316
OY 9149 CTTAAGCTCCGAGACGTGCATATTAATTAATTAATTAATTAATTAATTAATTAAT 9208
Db 7317 CTTAAGCTCCGAGACGTGCATATTAATTAATTAATTAATTAATTAATTAATTAAT 7376
OY 9209 TTTATTTACGTTGATATATATAGACAGTCAAGCGGTCCGTGATATGAGAGCGCGG 9268
Db 7377 TTTATTTACGTTGATATATATAGACAGTCAAGCGGTCCGTGATATGAGAGCGCGG 7436
OY 9269 TGCCTTAATAGAGATCGCCAGAGCGACAGATCTTCACTGTCTAGACAGGAGATAT 9328
Db 7437 TGCCTTAATAGAGATCGCCAGAGCGACAGATCTTCACTGTCTAGACAGGAGATAT 7496
OY 9329 GCGCACCGCTTCGTGACAGCGCGCGAGAGACAGTACGACCGCTAGCGCGCGCGCT 9388
|||||

Db 7497 GCGCACCGCTTCGTGACAGCGCGCGAGAGACAGTACGACCCCTAGCGCGCGCGCT 7556
OY 9389 ACTGCGCGGAGAGACGAAATTAACGGCGTGTGAGAGATCTGACCTTTAGAGAAA 9448
Db 7557 ACTGCGCGGAGAGAGAGAAATTAACGGCGTGTGAGAGATCTGACCTTTAGAGAAA 7616
OY 9449 CCGTGCAGCGGGGCAACATGGCCAGGAACTGCAAGATTTATACGCGAGCTGTGCG 9508
Db 7617 CCGTGCAGCGGGGCAACATGGCCAGGAACTGCAAGATTTATACGCGAGCTGTGCG 7676
OY 9509 CCGTGCAGCTTATGATCTGTATCTTTGGGAGCCCGGAGATATGAGCGGTGCGG 9568
Db 7677 CCGTGCAGCTTATGATCTGTATCTTTGGGAGCCCGGAGATATGAGCGGTGCGG 7736
OY 9569 CATTTTAAAAACAAAAACAGATAGAGAACCTGAACCGCGACCTTCTCGCTGTACG 9628
Db 7737 CATTTTAAAAACAAAAACAGATAGAGAACCTGAACCGCGACCTTCTCGCTGTACG 7796
OY 9629 CGAGCAAACTCGGTAGAGACGTCCAGCTGTGCTGAGAGTGGACACCTGGCAAAA 9688
Db 7797 CGAGCAAACTCGGTAGAGACGTCCAGCTGTGCTGAGAGTGGACACCTGGCAAAA 7856
OY 9689 CATCGAGCAAACTCGGGAGCTGGAGGCAAGTCTGGGCAAGATATTGACCGGAGA 9748
Db 7857 CATCGAGCAAACTCGGGAGCTGGAGGCAAGTCTGGGCAAGATATTGACCGGAGA 7916
OY 9749 GCATTTTGAACACTACCTGAGACCGCAATGTCACTATCACTTACGTTACTTTTCA 9808
Db 7917 GCATTTTGAACACTACCTGAGACCGCAATGTCACTATCACTTACGTTACTTTTCA 7976
OY 9809 GTTTTGGGGGGGGTTAATAGATTAATAGATTAATAGATTAATAGATTAATAGAT 9868
Db 7977 GTTTTGGGGGGGGTTAATAGATTAATAGATTAATAGATTAATAGATTAATAGAT 8036
OY 9869 GTGTAAAGACTAGGAGTGTGTATATGATGATGATGATGATGATGATGATGATGAT 9928
Db 8037 GTGTAAAGACTAGGAGTGTGTATATGATGATGATGATGATGATGATGATGATGAT 8096
OY 9929 GAACCGGTTCTGACGTTCTGTCAACACTGGGGGTATCTCCGATCCGACCCAGA 9988
Db 8097 GAACCGGTTCTGACGTTCTGTCAACACTGGGGGTATCTCCGATCCGACCCAGA 8156
OY 9989 CCTATACGTACAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 10048
Db 8157 CCTATACGTACAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8216
OY 10049 TCAGGGGTCAGTTTACTGCGCGTGTGCAACAGCAGACCTGCACTCACTGTAAAGA 10108
Db 8217 TCAGGGGTCAGTTTACTGCGCGTGTGCAACAGCAGACCTGCACTCACTGTAAAGA 8276
OY 10109 GGTAGGGCGGAGCCATACAGCGGCTGTTTGAAGACAGAACTGAGCCAGCTGGTAAA 10168
Db 8277 GGTAGGGCGGAGCCATACAGCGGCTGTTTGAAGACAGAACTGAGCCAGCTGGTAAA 8336
OY 10169 AGTAACAAACGTTGGAGCGCCAGCAGACGCGGTCCGCTCTGAGATCACTTAAAG 10228
Db 8337 AGTAACAAACGTTGGAGCGCCAGCAGACGCGGTCCGCTCTGAGATCACTTAAAG 8396
OY 10229 GAGTGTGCTGCGGGGCGCATACAGATCACTAATTAATTAATTAATTAATTAAT 10288
Db 8397 GAGTGTGCTGCGGGGCGCATACAGATCACTAATTAATTAATTAATTAATTAATTAAT 8456
OY 10349 CGAAACGAGTCTACAAATGGCCAGACTGTCTAACAACAGAGCGGATATGACAGACA 10408
Db 8517 CGAAACGAGTCTACAAATGGCCAGACTGTCTAACAACAGAGCGGATATGACAGACA 8576
OY 10409 CCGTGCAGCTAATTAACCCAAACTAAGCGCGCTACCTTACGACTTTTCCGACCGGA 10468
Db 8577 CCGTGCAGCTAATTAACCCAAACTAAGCGCGCTACCTTACGACTTTTCCGACCGGA 8636
|||||

OY	10469	TCCCATGAAATCCCTGTTCTTGCGGGCGGTCTTTTAACTCATAGACGACACCATAAACGC	10528
Db	8637	TCCCATGAAATCCCTGTTCTTGCGGGCGGTCTTTTAACTCATAGACGACACCATAAACGC	8696
OY	10529	ACTGAGCGGGGATTTGCTCCGCTGACGCTTTTCAACAGGGAACCTATACCAAGCTATGCG	10588
Db	8697	ACTGAGCGGGGATTTGCTCCGCTGACGCTTTTCAACAGGGAACCTATACCAAGCTATGCG	8756
OY	10589	AAAACAAAAGAGCTGTTCCACGACGATCAATAGCATCTCGCTGACGAGGAGCGCGGAGATC	10648
Db	8757	AAAACAAAAGAGCTGTTCCACGACGATCAATAGCATCTCGCTGACGAGGAGCGCGGAGATC	8816
OY	10649	GCAAAAACCGGGCCACCCCTTCGAGCCAGCGGACACCCACCTGTCGGCGCAACCGCGCAAG	10708
Db	8817	GCAAAAACCGGGCCACCCCTTCGAGGACCGGAGCACACCTGTCGGCGCAACCGCGCAAG	8876
OY	10709	GGAGCTCATCAAGAGACGACAGATATCGCAAAAGAAAGTACATGAAAAAAGTGGCCAGGGA	10768
Db	8877	GGAGCTCATCAAGAGACGACAGATATCGCAAAAGAAAGTACATGAAAAAAGTGGCCAGGGA	8936
OY	10769	CGGCTTTAAAAAATAACAGAGTGTCTGCAGACGCAAGACCGCGGTGTTGGCAACGCACAT	10828
Db	8937	CGGCTTTAAAAAATAACAGAGTGTCTGCAGACGCAAGACCGCGGTGTTGGCAACGCACAT	8996
OY	10829	CTGCAATCGGGGTATGGGGGGGGGCGCTATACGGCCGAGGGGTCCGACATGCTGTAACATTT	10888
Db	8997	CTGCAATCGGGGTATGGGGGGGGGCGCTATACGGCCGAGGGGTCCGACATGCTGTAACATTT	9056
OY	10889	TCTCTTCAGGCGGCGCTTCTGTCGCGCTCCCTGGGAGGCGCGCTGCGCTCGCATCAGAT	10948
Db	9057	TCTCTTCAGGCGGCGCTTCTGTCGCGCTCCCTGGGAGGCGCGCTGCGCTCGCATCAGAT	9116
OY	10949	TTTATTTGAAAACTCAAGTACATTTAAAAAATCTACATATATCTCCACGCGCTCAATCGGGA	11008
Db	9117	TTTATTTGAAAACTCAAGTACATTTAAAAAATCTACATATATCTCCACGCGCTCAATCGGGA	9176
OY	11009	ACAGGTAGAGATTATACGCTGAGATTTTACGCGCTGATTAACCGCGCGCCCTACAGCGCCA	11068
Db	9177	ACAGGTAGAGATTATACGCTGAGATTTTACGCGCTGATTAACCGCGCGCCCTACAGCGCCA	9236
OY	11069	GAGCGATCTCTTTCGCCGGCCCCGCCCAACGTCGCGCTGCGCCAGTGTTTGAGAGCGCGCG	11128
Db	9237	GAGCGATCTCTTTCGCCGGCCCCGCCCAACGTCGCGCTGCGCCAGTGTTTGAGAGCGCGCG	9296
OY	11129	AATGCTTCCGATCACAAAGATGCGGGGTAGAGATGATATGGCCCCACATTCACACGGA	11188
Db	9297	AATGCTTCCGATCACAAAGATGCGGGGTAGAGATGATATGGCCCCACATTCACACGGA	9356
OY	11189	AGACTGATAGACGACATTTAATCGTTTTTACCAACTTCCCGAAGTGATCTCAACGC	11248
Db	9357	AGACTGATAGACGACATTTAATCGTTTTTACCAACTTCCCGAAGTGATCTCAACGC	9416
OY	11249	GGTCAAAAAGTCCGCGCTGCTGCTTATACAGAGCGTCGTCCTCGCTGGCGCTTATATA	11308
Db	9417	GGTCAAAAAGTCCGCGCTGCTGCTTATACAGAGCGTCGTCCTCGCTGGCGCTTATATA	9476
OY	11309	TCGCAAGCTGGAAAAAGACGCTGGGGAATTTTCCCTAGGCGCGGAGAAACTCTCCATCTC	11368
Db	9477	TCGCAAGCTGGAAAAAGACGCTGGGGAATTTTCCCTAGGCGCGGAGAAACTCTCCATCTC	9536
OY	11369	CAACCTAGAGCTTAAAGGCTGACGTCGCGCTGTATCTAAGCTACGACCAAGACGCGCC	11428
Db	9537	CAACCTAGAGCTTAAAGGCTGACGTCGCGCTGTATCTAAGCTACGACCAAGACGCGCC	9596
OY	11429	GCTGCTTCAATTTCTCAAAATACCGGCTGGATATTAAAGACCTTACGCTTCTCTGA	11488
Db	9597	GCTGCTTCAATTTCTCAAAATACCGGCTGGATATTAAAGACCTTACGCTTCTCTGA	9656
OY	11489	CCATTCACCTGCACGTGCGAGCGCAATGATGATTAACCGAACGCGTCTCTCTGC	11548
Db	9657	CCATTCACCTGCACGTGCGAGCGCAATGATGATTAACCGAACGCGTCTCTCTGC	9716

QY	11549	GGCGCTGGGTGATATATCGCATGCGGACGCGCGTGGCGAAATGTCACACCOC	11608
Db	9717	GGGGGTGGGTGATATATCGCATGCGGACGCGCGTGGCGAAATGTCACACCOC	9776
QY	11609	AGGGCGGACACACCGCGACGCAAGCGCGGGCCGTGACAGCCACACCTCCGANA	11668
Db	9777	AGGGCGGACACACCGCGACGCAAGCGCGGGCCGTGACAGCCACACCTCCGANA	9836
QY	11669	ACCCACCTAAGGGCGGAGCGCTTTAAAGTTTGGCTGTGACAGCGCTGGCGACGGGANA	11728
Db	9837	ACCCACCTAAGGGCGGAGCGCTTTAAAGTTTGGCTGTGACAGCGCTGGCGACGGGANA	9896
QY	11729	TCCTTCAGGTTTAACTTGGAATAAAGTGTCGGGCGACCGAGACAAGACCAAGAAG	11788
Db	9897	TCCTTCAGGTTTAACTTGGAATAAAGTGTCGGGCGACCGAGACAAGACCAAGAAG	9956
QY	11789	GCATTCGATGTGTTTAAAAAAATATTTGTCCCCGCACATCTTTAAGGTCAACG	11848
Db	9957	GCATTCGATGTGTTTAAAAAAATATTTGTCCCCGCACATCTTTAAGGTCAACG	10016
QY	11849	GCAAGGTGGCCACCTCGGTGACCGTCTATGAGAGGTGGACCGGACCGCGTAGCCGGA	11908
Db	10017	GCAAGGTGGCCACCTCGGTGACCGTCTATGAGAGGTGGACCGGACCGCGTAGCCGGA	10076
QY	11909	AGCAAGAGTTCATCCGACCGGTGCGCGCATGACAGATCAACCAATGACAGACCTTACC	11968
Db	10077	AGCAAGAGTTCATCCGACCGGTGCGCGCATGACAGATCAACCAATGACAGACCTTACC	10136
QY	11969	AGTGTTCAGTCCATCGCGGTAAACGTCAACGGCATATGTAACACCTTACAGGACAGG	12028
Db	10137	AGTGTTCAGTCCATCGCGGTAAACGTCAACGGCATATGTAACACCTTACAGGACAGG	10196
QY	12029	ACCTTCACATAACCAACACGCTGTTTCTGCAACCGGTGCGAGGGGCTCAGCGATTAATCATCAGC	12088
Db	10197	ACCTTCACATAACCAACACGCTGTTTCTGCAACCGGTGCGAGGGGCTCAGCGATTAATCATCAGC	10256
QY	12089	GATACCTTCAGTCAGCCGGTCTGTACAACGACACCGGATGTGTTCCGGAAATTTACAGGG	12148
Db	10257	GATACCTTCAGTCAGCCGGTCTGTACAACGACACCGGATGTGTTCCGGAAATTTACAGGG	10316
QY	12149	TCACAACACGCGTAACTGCGAGATGCTGGACATGATCGCGCTTGGCGGAAACGCTACT	12208
Db	10317	TCACAACACGCGTAACTGCGAGATGCTGGACATGATCGCGCTTGGCGGAAACGCTACT	10376
QY	12209	CGTATTTTGTACACGCCCTGGGAGACACGGTAGGGGTGCCGTTCTGCCAACAACGACT	12268
Db	10377	CGTATTTTGTACACGCCCTGGGAGACACGGTAGGGGTGCCGTTCTGCCAACAACGACT	10436
QY	12269	CAACGTGCTCGTGGCGGAGAAACCCAAACACGGCGCTCGGCGCCCGCTGCTACAAATTT	12328
Db	10437	CAACGTGCTCGTGGCGGAGAAACCCAAACACGGCGCTCGGCGCCCGCTGCTACAAATTT	10496
QY	12329	ACACCATGTCGACTTGCGACGCCCGCCAGCCACACCGAAGCGGGTCTTGCGCGACT	12388
Db	10497	ACACCATGTCGACTTGCGACGCCCGCCAGCCACACCGAAGCGGGTCTTGCGCGACT	10556
QY	12389	CGGAGAGATACACCGTATACGTGGAAGGCGGAGAACCCCAAGTGGGGGTCTGCGCGCTA	12448
Db	10557	CGGAGAGATACACCGTATACGTGGAAGGCGGAGAACCCCAAGTGGGGGTCTGCGCGCTA	10616
QY	12449	CGCTCTGGAATAACCTTCCCGAGGGCGATACAGACGACGACGAGCGACGTACACTTGG	12508
Db	10617	CGCTCTGGAATAACCTTCCCGAGGGCGATACAGACGACGACGAGCGACGTACACTTGG	10676
QY	12509	TGGCCAAACGATGACGGCGACTTTCACGTCCCGCTCTCCAGGTAACTAACTTACGG	12568
Db	10677	TGGCCAAACGATGACGGCGACTTTCACGTCCCGCTCTCCAGGTAACTAACTTACGG	10736
QY	12569	GCAGTACCCCTGGCTCAATGATGTTTATGGAATAACCTTCAACGCGACACTTCAAGACA	12628
Db	10737	GCAGTACCCCTGGCTCAATGATGTTTATGGAATAACCTTCAACGCGACACTTCAAGACA	10796
QY	12629	TGTCGATATCCACGACAACCGATTCGGAGAGTACTTCGAACCCGAGGGGGTCTGT	12688

Db 10797 TGTCTGATACACATGTGTGCAAAAGGGGTGGCCGAGTACTACAGACAGAAAGGGGGCTGT 10856
Qy 12689 TTCTCTGTGTGGACCGGTTAAAGCGCGCTTAAGCCTAGCTAGGAGATGGCGCAATTAACG 12748
Db 10857 TTCTACTGTGTGACGCGGTTAAAGCGCCCTGAGCCTGTGTGAGGAATGGCGGCTTAACG 10916
Qy 12749 GCACACGCGCCAGCAACCCCGCCACCAACCTCAACCGCCCAACCGGTTGGAAGAGCGTCG 12808
Db 10917 GCACACGCGCCAGCAACCCCGCCACCTCAACCGCTCAACCGCGGTTGTGGAAGAGCTTA 10976
Qy 12809 GTACGAACGAGCAGCAAGCGAGCAACCTAGCGGCGCCCAAGTCTAGTTCGCTACAGCA 12868
Db 10977 ATAGCAAGGAGCAGCAAGCAACTGTGAGCGCCCGCAAGTTCGCTACAGCA 11036
Qy 12869 AGCTCCGCGCGAGCATCAACAAGGTGTGAGAGACTCTCCAGGGCGTGTGTGCCAGAAC 12928
Db 11037 AACTACGCGCGAGCATCAACAAGGTGTGAGAGACTCTCCAGGGCGTGTGTGCCAGAAC 11096
Qy 12929 AGGTGAGGAGCAACCTACATGTGTGTGAGCACTGAGCAAGATTAAACCCACAGCCTAATGA 12988
Db 11097 AGGTGAGGAGCAACCTACATGTGTGTGAGCACTGAGCAAGATTAAACCCACAGCCTAATGA 11156
Qy 12989 CGCGGATATACGGGCGCGGCTGTGCGCAAGTTCGTGGGGAGCGCATGCGGTGACGG 13048
Db 11157 CAGGATATACGGGCGCGGCTGTGCGCAAGTTCGTGGGGAGCGCATGCGGTGACGG 11216
Qy 13049 ACTGCTGGCGGTGGAGCAGGCGTCCGTACAGCATCAACAAGCCTCCGACGTCACCC 13108
Db 11217 ACTGCTGGCGGTGGAGCAGGCGTCCGTACAGCATCAACAAGCCTCCGACGTCACCC 11276
Qy 13109 CGGGGATCTGCTACTCGCGGCGCCCGGTCACGTTCAAGTTCCTTAACAGCACACGCTGT 13168
Db 11277 CGGGAAATGTCTACTCGCGGCGCCCGGTCACGTTCAAGTTCCTTAACAGCACACGCTGT 11336
Qy 13169 TCAAGGGCCAGCTGGGACCCAGAAAGAGATCATCTAGCAGCAACAGCAGGTGGAGGCGT 13228
Db 11337 TCAAGGGCCAGCTGGGACCCAGAAAGAGATCATCTAGCAGCAACAGCAGGTGGAGGCGT 11396
Qy 13229 GCAAAAGAGAGCTGGCAACACTACTTCAATAGCAGCAACAGTACCTACTACTACAAAGACT 13288
Db 11397 GCAAAAGAGAGCTGGCAACACTACTTCAATAGCAGCAACAGTACCTACTACTACAAAGACT 11456
Qy 13289 ACGTCTCTGAAAAAAATTAACACCTCGAGATATCCGAGATATCCGAGTCTCATCGCCC 13348
Db 11457 ACGTCTCTGAAAAAAATTAACACCTCGAGATATCCGAGATATCCGAGTCTCATCGCCC 11516
Qy 13349 TGAACCTGTGTTATAGAGACATAGATTTCAGGGTCAATCGAGCTGTACAGCGCGCG 13408
Db 11517 TGAACCTGTGTTATAGAGACATAGATTTCAGGGTCAATCGAGCTGTACAGCGCGCG 11576
Qy 13409 AGAAAAAGCTGTCCGGGAGCGTTTGTGATATAGAAACCATGTTACAGGAATACAACTACT 13468
Db 11577 AGAAAAAGCTGTCCGGGAGCGTTTGTGATATAGAAACCATGTTACAGGAATACAACTACT 11636
Qy 13469 ACACGCAACGCTGGGGGAGCTCGGGAGAGACTGGACACAGACATGCAACCTCAACCGCG 13528
Db 11637 ACACGCAACGCTGGGGGAGCTCGGGAGAGACTGGACACAGACATGCAACCTCAACCGCG 11696
Qy 13529 ACCGCGTGGCGCCGAGACTGTCCGAGATAGTCCGGAGCTGGGCGATGTGCGCGCACGG 13588
Db 11697 ACCGCGTGGCGCCGAGACTGTCCGAGATAGTCCGGAGCTGGGCGATGTGCGCGCACGG 11756
Qy 13589 TCGTTAAACGTGGCCAGTAGCGGTATACCTGTTCGGATCAATCGTAGCGGGTTCAATTA 13648
Db 11757 TCGTTAAACGTGGCCAGTAGCGGTATACCTGTTCGGATCAATCGTAGCGGGTTCAATTA 11816
Qy 13649 ACTTTAAAGAGTCCGTTCCGGGGGATGCTCATGTATCTCGTGATTTGGGGCGTGTCTC 13708
Db 11817 ACTTTAAAGAGTCCGTTCCGGGGGATGCTCATGTATCTCGTGATTTGGGGCGTGTCTC 11876
Qy 13709 TGAATCGTTGTGGCTAAACCGGCGCACCAACGCCATCGCCAGGCGCCCATCAGATGA 13768
|||||

Db 11877 TGAATCGTTGTGGCTAAACCGGCGCACCAACGCCATCGCCAGGCGCCCATCAGATGA 11936
Qy 13769 TCTACCCCGACATATAGACAAAATGACGCCCTCTGTGGCGGTAAAGTGCACAGAGACAGATTA 13828
Db 11937 TCTACCCCGACATATAGACAAAATGACGCCCTGTGGCGGTAAAGTGCACAGAGACAGATTA 11996
Qy 13829 AAAACATTTCTCGCGGATGACACAGCTACAGCAGAGAAAGCGTAGCGGTTAGAGCAAC 13888
Db 11997 AAAACATTTCTCGCGGATGACACAGCTACAGCAGAGAAAGCGTAGCGGTTAGAGCAAC 12056
Qy 13889 AGCAGAGTACAGGCGCCCTCTGCTTTTCGGGGCGGTGACAGAGGACTTAAAGTGCAGTTTA 13948
Db 12057 AGCAGAGTACAGGCGCCCTCTGCTTTTCGGGGCGGTGACAGAGGACTTAAAGTGCAGTTTA 12116
Qy 13949 GGGGATATTAACCGCTTGAAAAAGAGGCTCAAGAGTATGAATGACAAATTAACAC 14008
Db 12117 GGGGATATTAACCGCTTGAAAAAGAGGCTCAAGAGTATGAATGACAAATTAACAC 12176
Qy 14009 ACCCACACGCTGTACTTGTCCGCGCCGACAGACCGCGCGCCCAATGATTTGCGCACCG 14068
Db 12177 ACCCACACGCTGTACTTGTCCGCGCCGACAGACCGCGCGCCCAATGATTTGCGCACCG 12236
Qy 14069 GCGGTCGCCGACACCTTATAGGCGCCCGGGGGTCCGGGCTGTATCAATCATGGATT 14128
Db 12237 GCGGTCGCCGACACCTTATAGGCGCCCGGGGGTCCGGGCTGTATCAATCATGGATT 12296
Qy 14129 TCTTTAACCCGCTACTGTGGGCCCTTCGGGAGACAGACGCCCCCACTACACAGAGCACCGATG 14188
Db 12297 TCTTTAACCCGCTACTGTGGGCCCTTCGGGAGACAGACGCCCCCACTACACAGAGCACCGATG 12356
Qy 14189 CTCGCCGCCCTGCGCGGCGCGGAGCGTTTACGCCGACACAGACGTTTGGAGGCTCATCC 14248
Db 12357 CTCGCCGCCCTGCGCGGCGCGGAGCGTTTACGCCGACACAGACGTTTGGAGGCTCATCC 12416
Qy 14249 CCGCCTGCTCTCCGAACGCCGAGGGGAGGGGGATGATCCGGTCAAGATCCGTTCCCG 14308
Db 12417 CCGCCTGCTCTCCGAACGCCGAGGGGAGGGGGATGATCCGGTCAAGATCCGTTCCCG 12476
Qy 14309 CAACGTACTTGAAGAACGGTGTCCGGAGAGCTGTGCTGCTCGCAACGAAGGTCATGT 14368
Db 12477 CAACGTACTTGAAGAACGGTGTCCGGAGAGCTGTGCTGCTCGCAACGAAGGTCATGT 12536
Qy 14369 GGAAGCGCGCGGAGCCGCAAGCCCGTGGCCCGGACCCCAAGACCAATCATACGTTTC 14428
Db 12537 GGAAGCGCGCGGAGCCGCAAGCCCGTGGCCCGGAGCCCAAGACCAATCATACGTTTC 12596
Qy 14429 ACGGTAACGACGTGTGTAACCAACGTACGCGGCGGAGACAGGTGTGCGGAGTACCTAGGC 14488
Db 12597 ACGGTAACGACGTGTGTAACCAACGTACGCGGCGGAGACAGGTGTGCGGAGTACCTAGGC 12656
Qy 14489 GCTTCCAAACGGACATTTATCCCAAGCGGAACCGTGTCAAGCTCTGGGGCGAACCAGAG 14548
Db 12657 GCTTCCAAACGGACATTTATCCCAAGCGGAACCGTGTCAAGCTCTGGGGCGAACCAGAG 12716
Qy 14549 ACGGCAACGAGCGTGTGTAACGTTTCCGTCACAAAGTATTTCTACGGAAGTTTC 14608
Db 12717 ACGGCAACGAGCGTGTGTAACGTTTCCGTCACAAAGTATTTCTACGGAAGTTTC 12776
Qy 14609 CAGCGCGATTAACGTACACCCACATCTCCAGAGGCGCTCAAGAAACACAGCGCGGCGTG 14668
Db 12777 CAGCGCGATTAACGTACACCCACATCTCCAGAGGCGCTCAAGAAACACAGCGCGGCGTG 12836
Qy 14669 CCGCGTGGCGGCTTTCGACAGAGAGTGAACAAAAGATTTCTCAAAAGCTACGAGCTG 14728
Db 12837 CCGCGTGGCGGCTTTCGACAGAGAGTGAACAAAAGATTTCTCAAAAGCTACGAGCTG 12896
Qy 14729 CGGAGATCCCGTCAAGGAAATCAGGCTATCGTCCGGTTCCATGCTCTGACACCTACAGC 14788
Db 12897 CGGAGATCCCGTCAAGGAAATCAGGCTATCGTCCGGTTCCATGCTCTGACACCTACAGC 12956
Qy 14789 ACCGCTCTGCGCGGCGGCTGAGAGTTTGGAGTCAAAACGTGAGCGCGCTTCCCGGT 14848
Db 12957 ACCGCTCTGCGCGGCGGCTGAGAGTTTGGAGTCAAAACGTGAGCGCGCTTCCCGGT 13016
|||||

14849 TCGTTCGATCAAGGGTTTACGACGTTCCGGTGGTACTGTCGGCGCGCCGACGCC 14908
13017 TCGTTCGATCAAGGGTTTACGACGTTCCGGTGGTACTGTCGGCGCGCGCCGACGCC 13076
14909 GCGTCGGCGGACAGATGCGACGAGCGCCCTGGAGTTTGACTGCACTGGGAGACCTCA 14968
13077 GCGTCGGCGGACAGATGCGACGAGCGCCCTGGAGTTTGACTGCACTGGGAGACCTCA 13136
14969 GCGTCGAAGGGACCGGACGACTGCGCCCGGACCGCATCGTGGCTTTGATATCGAGT 15028
13137 GCGTCGAAGGGACCGGACGACTGCGCCCGGACCGCATCGTGGCTTTGATATCGAGT 13196
15029 GCACTGGAGAGCGGGATTTCCGTGCGCACGCGCGACGCGCGATGATCGATCT 15088
13197 GCACTGGAGAGCGGGATTTCCGTGCGCACGCGCGACGCGCGATGATCGATCT 13256
15089 CCGTCGCTCTTACACGACGAGGAGGCGGCCCAATCCGCCAATACCTGTTGACGC 15148
13257 CCGTCGCTCTTACACGACGAGGAGGCGGCCCAATCCGCCAATACCTGTTGACGC 13316
15149 TCGGAGAGTGGACCCGATCCCGGACGCGAGCTTTGAGTTCCGTGGGAATATGACA 15208
13317 TCGGAGAGTGGACCCGATCCCGGACGCGAGCTTTGAGTTCCGTGGGAATATGACA 13376
15209 TCGTGTGTGCTCTTCCGATGATCCGACATTCGAGCTTGAAGCTTTTAAACGGCTATA 15268
13377 TCGTGTGTGCTCTTCCGATGATTCGCGACATTCGAGTGGATTTTAAACGGCTATA 13436
15269 ACATCTCAAACTTCGATCTCCGTAATACACGCGAGCTCCGACGATCAACCTTC 15328
13437 ACATCTCAAACTTCGATCTCCGTAATACACGCGCTCCGACGATCAACCTTC 13496
15329 GATTAAAGCAATACAAATAATAAACCAGCTCCATCTTGAAGTTACAGAGCCCGTG 15388
13497 GATTAAAGCAATACAAATAATAAACCAGCTCCATCTTGAAGTTACAGAGCCCGTG 13556
15389 GCGGGGAGGGGGTTTCATGAGTCCGCTCAAAAATTAATAATAGCGGATCTCCCA 15448
13557 GCGGGGAGGGGGTTTCATGAGTCCGCTCAAAAATTAATAATAGCGGATCTCCCA 13616
15449 TAGACATGTACACAGGTGTGTCGCAAAAAGCTCAACCTCCGATACAACTGGACACG 15508
13617 TAGACATGTACACAGGTGTGTCGCAAAAAGCTCAACCTCCGATACAACTGGACACG 13676
15509 TGGCGAGGCAAGTGTGGGTGGGAAAAAGAGCAAGTATGTACAAAGCAATCCCTC 15568
13677 TGGCGAGGCAAGTGTGGGTGGGAAAAAGAGCAAGTATGTACAAAGCAATCCCTC 13736
15569 TGTTCGCTAGAGTCCGGGGGAGGCTAAGGTGAGGCTATTTGCTGATGACCTCG 15628
13737 TGTTCGCTAGAGTCCGGGGGAGGCTAAGGTGAGGCTATTTGCTGATGACCTCG 13796
15629 TCCTGTGATGACCTCTTAAAAATGTTATGATACAGTGGAGATTTCGGAGATACCA 15688
13797 TCCTGTGATGACCTCTTAAAAATGTTATGATACAGTGGAGATTTCGGAGATACCA 13856
15689 AGCTGGCAAGATTCAAGGCGGCGCTGACAGGCGCAACACTCCGCTGTTCT 15748
13857 AGCTGGCAAGATTCAAGGCGGCGCTGACAGGCGCAACACTCCGCTGTTCT 13916
15749 CTTGCTGTGAGAGCGCGGCGAGGAGAACTTTATCTCCGGTTTCAACGCGCGAG 15808
13917 CTTGCTGTGAGAGCGCGGCGAGGAGAACTTTATCTCCGGTTTCAACGCGCGAG 13976
15809 GACAGGGGGCTATCAGGGCGGACGAGTATCAACCCATTCGCGGGTTTACGACGAGC 15868
13977 GACAGGGGGCTATCAGGGCGGACGAGTATCAACCCATTCGCGGGTTTACGACGAGC 14036
15869 CGGTCTGTGTGATGATTTTCCAGCTGTATCCGAGACATCATCCAGGCGCAACCTGT 15928
14037 CGGTCTGTGTGATGATTTTCCAGCTGTATCCGAGACATCATCCAGGCGCAACCTGT 14096

15929 GCTACTCCACCATGATATACAGGAGAGACCTGCACACTGCACCCCAACCTGACCGGACG 15988
14097 GCTACTCCACCATGATATACAGGAGAGACCTGCACACTGCACCCCAACCTGACCGGACG 14156
15989 ACTACGAGAGCTTCTGCTCAAGCGGCGGACCGGTACATTTTGTAAAAAACACAGCGGG 16048
14157 ACTACGAGAGCTTCTGCTCAAGCGGCGGACCGGTACATTTTGTAAAAAACACAGCGGG 14216
16049 AGTCTGTGGGGAGAGCTGTAAACGCTGTGGTTAGAAAAAGCGAAGGGGATCCGGGCA 16108
14217 AGTCTGTGGGGAGAGCTGTAAACGCTGTGGTTAGAAAAAGCGAAGGGGATCCGGGCA 14276
16109 CCGTGGCGGCTGCGATGACCCGCTGCTAAAAAACCATCTTATAGATTAACAACAGCTGGCA 16168
14277 CCGTGGCGGCTGCGATGACCCGCTGCTAAAAAACCATCTTATAGATTAACAACAGCTGGCA 14336
16169 TCAAGTGAATGTATACCGGCTTACCGGTTACACCGGGTGGCCAGCGGCTCTCCAT 16228
14337 TCAAGTGAATGTATACCGGCTTACCGGTTACACCGGGTGGCCAGCGGCTCTCCAT 14396
16229 GCATTAACATAGCGGAAACCGTGAAGCTCCGGGGGCGCACGATGCTGAGATGTCAAGT 16288
14397 GCATTAACATAGCGGAAACCGTGAAGCTCCGGGGGCGCACGATGCTGAGATGTCAAGT 14456
16289 CTTACGTGAGAGCCCTGACGACGAGAACCTGCGAACGCTCTCGTCCGAGGTGACG 16348
14457 CTTACGTGAGAGCCCTGACGACGAGAACCTGCGAACGCTCTCGTCCGAGGTGACG 14516
16349 CCGGTCAAGCGGCGGCTTTCGCTGCTTACGCTGACACCGACTCCCTTTATCGCGT 16408
14517 CCGGTCAAGCGGCGGCTTTCGCTGCTTACGCTGACACCGACTCCCTTTATCGCGT 14576
16409 GCGACGGTTATTCGCGGAAAGCGGTTCCGGTTCTGTGACGATCTGCGCGCAGATCA 16468
14577 GCGACGGTTATTCGCGGAAAGCGGTTCCGGTTCTGTGACGATCTGCGCGCAGATCA 14636
16469 CTGCGGACCTGTTCCGCCCAACCTTAAGCTAGAGGCGGAAAGACGTTCAAGTGTGC 16528
14637 CTGCGGACCTGTTCCGCCCAACCTTAAGCTAGAGGCGGAAAGACGTTCAAGTGTGC 14696
16529 TGTGCTGACGAAAAACCGCTACTTCGGGCTCTATTGAAACGACAAAAATGTCATGAAG 16588
14697 TGTGCTGACGAAAAACCGCTACTTCGGGCTCTATTGAAACGACAAAAATGTCATGAAG 14756
16589 GGGTCGACCTCATTCGCAAAAACCGCTGCAAGTTGTGCAAGGACGATGCGGCGCATTC 16648
14757 GGGTCGACCTCATTCGCAAAAACCGCTGCAAGTTGTGCAAGGACGATGCGGCGCATTC 14816
16649 TGGACCTGTGCTTCACAGATCCGAGGTCAAGGCTGCGGCGCGCTGTTGTGAAGCGGC 16708
14817 TGGACCTGTGCTTCACAGATCCGAGGTCAAGGCTGCGGCGCGCTGTTGTGAAGCGGC 14876
16709 CGCCGACGCGGTATACGAGAGGGGCTCCGCGCTGCTTTATAAAAATGCTAGAGTCC 16768
14877 CGCCGACGCGGTATACGAGAGGGGCTCCGCGCTGCTTTATAAAAATGCTAGAGTCC 14936
16769 TCAACGGAGGTATCTGAGACTCCGAAACAGCGCTGCGCCATGAGACAGATTACGTTCT 16828
14937 TCAACGGAGGTATCTGAGACTCCGAAACAGCGCTGCGCCATGAGACAGATTACGTTCT 14996
16829 CCAACGAGCTCAGCGCGCGCTGCGATTACAAGACCAACCACTCCGACCTGCGG 16888
14997 CCAACGAGCTCAGCGCGCGCTGCGATTACAAGACCAACCACTCCGACCTGCGG 15056
16889 TGTACCAAAAAGCTGCGACGAGCTGCGAGAGCTGCCCAAGTGCACGATAGAAATCCCT 16948
15057 TGTACCAAAAAGCTGCGACGAGCTGCGAGAGCTGCCCAAGTGCACGATAGAAATCCCT 15116
16949 ACGTGTCTGTTGAGCGCGCGGCTCCTAAAGTGGACCTGCGGCAACCCGATTAAG 17008
15117 ACGTGTCTGTTGAGCGCGCGGCTCCTAAAGTGGACCTGCGGCAACCCGATTAAG 15176
17009 TCAAGACGACCAAGATTCCCGTCCGCGTGCACCTATATTTCGACAAACTGGTGCACGCG 17068

Db 15177 TCAGACGACACGATTCCTCGCGGTGACCTATATTTTCGACAACTGTGTACGGCG 15236
QY 17069 CGGCGCAACATCTCTCACTGTCTGTTCGGCAACAACGGGACACACAGGATGGCCATCTT 17128
Db 15237 CGGCGCAACATCTCTCACTGTCTGTTCGGCAACAACGGGACACACAGGATGGCCATCTT 15296
QY 17129 ACAATTTTTCACAGCTCCCGTATTAAGCTGTTCGTGTGACGCCAATTTGAGAACGCCAAC 17188
Db 15297 ACAATTTTTCACAGCTCCCGTATTAAGCTGTTCGTGTGACGCCAATTTGAGAACGCCAAC 15356
QY 17189 ATAGAAGCGCGCGACGGGAGTCCGAGGAGAGGCTCGAGGGGCGAGGCGGACCAACG 17248
Db 15357 ATAGAAGCGCGCGCGACGGGAGTCCGAGGAGAGGCTCGAGGGGCGAGGCGGACCAACG 15416
QY 17249 GAGACCGCCACCATGTGTGTTAAAGAACTGTCTGTGTGCTCGGCGCTGGAGAGTACT 17308
Db 15417 GAGACCGCCACCATGTGTGTTAAAGAACTGTGTGTGTCTGTGTGTGTGTGTGTGTGTGT 15476
QY 17309 TTTTACCGGGGGTATGATTCAGCTTCGTACCTTACCCGCTGCAAAAGTTCAAGGGCCAC 17368
Db 15477 TTTTACCGGGGGTATGATTCAGCTTCGTACCTTACCCGCTGCAAAAGTTCAAGGGCCAC 15536
QY 17369 GGGGGCTACGACGAGGGGCTGACCTCCCTTCTGCTGACAGTTACCCACCAACATTTTC 17428
Db 15537 GGGGGCTACGACGAGGGGCTGACCTCCCTTCTGCTGACAGTTACCTCCACCAACATTTTC 15596
QY 17429 GCGTTTGGAGCTGTGACGGGTCTCAAGAACTGCCCCCTTCTCCGACTGCGTGGCCCTT 17488
Db 15597 GCGTTTGGAGCTGTGACGGGTCTCAAGAACTGCCCCCTTCTCCGACTGCGTGGCCCTT 15656
QY 17489 ATGCGCCCGTTGGATTCGCGCGCGGCGACGGGAGAGCGGGCGCGCTGGCCCGCGGTTCTG 17548
Db 15657 ATGCGCCCGTTGGATTCGCGCGCGGCGACGGGAGAGCGGGCGCGCTGGCCCGCGGTTCTG 15716
QY 17549 CTGAGCTCTCTCTGCGCGCTGACCGTGTGGGTAAAGCGGAGCGGGCGGACACAGATCCG 17608
Db 15717 CTGAGCTCTCTCTGCGCGCGTGAACCGTGTGGGTAAAGCGGAGCGGGCGGACACAGATCCG 15776
QY 17609 TTTTGGCTCTCTCTTTTAAAGCCGATGACCTGTGAGCGCGCGGTCAAGTACGTCTTCTG 17668
Db 15777 TTTTGGCTCTCTCTTTTAAAGCCGATGACCTGTGAGCGCGCGGTCAAGTACGTCTTCTG 15836
QY 17669 GAGAACGGGCGCGCGCTGCGGAGGCGACCCCAACCGGCGGCGGACCCGAAACCGT 17728
Db 15837 GAGAACGGGCGCGCGCTGCGGAGGCGACCCCAACCGGCGGCGGACCCGAAACCGT 15896
QY 17729 CCGGCTGGAACCCCTGCGCTCTCCGCGAGGGGTCTCAAGCTGCGCCATTTCTTCTG 17788
Db 15897 CCGGCTGGAACCCCTGCGCTCTCCGCGAGGGGTCTCAAGCTGCGCCATTTCTTCTG 15956
QY 17789 GCGTATTTTTCACAGCGGCACTGCTGTGCGCTTAAAGCTGTGCGGTTTACAGTGAAG 17848
Db 15957 GCGTATTTTTCACAGCGGCACTGCTGTGCGCTTAAAGCTGTGCGGTTTACAGTGAAG 16016
QY 17849 CCGTATTTTTCAGAGCGGCGGACAGGAGGCGGCGGATCTCCCGGAAATACGACAGTT 17908
Db 16017 CCGTATTTTTCAGAGCGGCGGACAGGAGGCGGCGGATCTCCCGGAAATACGACAGTT 16076
QY 17909 AGTAATCTCGGGGGTAACTGTGCAAGGGGTCTGCTTCAACAGCTGCGCGCTGCGGCT 17968
Db 16077 AGTAATCTCGGGGGTAACTGTGCAAGGGGTCTGCTTCAACAGCTGCGCGCTGCGGCT 16136
QY 17969 AAAAGCGCGCAATGGAATCTATCTACGCTCCCGGGGACCCCAAGCGCGAGATAGTCTG 18028
Db 16137 AAAAGCGCGCAATGGAATCTATCTACGCTCCCGGGGACCCCAAGCGCGAGATAGTCTG 16196
QY 18029 GGGCGGTGCGGAGCGCTCTGCGCAACCGGACAGCGGGCGGGGTATGGGGGTCTACGCC 18088
Db 16197 GGGCGGTGCGGAGCGCTCTGCGCAACCGGACAGCGGGCGGGGTATGGGGGTCTACGCC 16256
QY 18089 GAGCGCGAAAAACCATCCATCCTGGAAGCTCCGCGGAGTCCGGGTAGTTAATCTTC 18148
|||||

Db 16257 GAGCGCGAAAAACCATCCATCCTGGAAGCTCCGCGGAAAGTCCGGTTAGTTAATCTTC 16316
QY 18149 CAACAGGAGAGCGCGCTCTGCGGCGGATGTGGCGTTTCTGTGTCAGGGGCGTGGACCGGAG 18208
Db 16317 CAACAGGAGAGCGCGCTCTGCGGCGGATGTGGCGTTTCTGTGTCAGGGGCGTGGACCGGAG 16376
QY 18209 CCGCTATTGCTGCTCACCCCGGACACTTGTCTTCCGTTTGCACAAACCACTGCGCTTA 18268
Db 16377 CCGCTATTGCTGCTCACCCCGGACACTTGTCTTCCGTTTGCACAAACCACTGCGCTTA 16436
QY 18269 TTACACCCCAAGCGTACCCCGACGACTATTAAGAGACACCTTGTGGCGCGCGCGG 18328
Db 16437 TTACACCCCAAGCGTACCCCGACGACTATTAAGAGAGACACCTTGTGGCGCGCGCGG 16496
QY 18329 CCCTGCGCGGTGTGCGATTAAGCTCTCGCGGACGAGCGCGCGGAGACCTGTGCGCTTA 18388
Db 16497 CCCTGCGCGGTGTGCGATTAAGCTCTCGCGGACGAGCGCGCGGAGACCTGTGCGCTTA 16556
QY 18389 CCAGACACCGGGGCGCTCTCCATTAACGCGTTTACATCCCGTGTGTTCCAGGGGTG 18448
Db 16557 CCAGACACCGGGGCGCTCTCCATTAACGCGTTTACATCCCGTGTGTTCCAGGGGTG 16616
QY 18449 GTCTGGCGGAGTGTACGCTGCTTACGCGAACGAGGGGTCCAGCAACGATTAACAT 18508
Db 16617 GTCTGGCGGAGTGTACGCTGCTTACGCGAACGAGGGGTCCAGCAACGATTAACAT 16676
QY 18509 TGAACGCAACGATGGGAGAACCGGTGCTGTTTCTTTCGCGGCGAGTGGACCTCGAGTC 18568
Db 16677 TGAACGCAACGATGGGAGAACCGGTGCTGTTTCTTTCGCGGCGAGTGGACCTCGAGTC 16736
QY 18569 TAGTGGACAAAGGAGAACCGGCTACGCTCCCTGTGTGTGGGCGGCTACATTTACAGAC 18628
Db 16737 TAGTGGACAAAGGAGAACCGGCTACGCTCCCTGTGTGTGGGCGGCTACATTTACAGAC 16796
QY 18629 GCTACCTGACACTGTGGAACAGTGTGAGCTGTGCTACGAGAGAGTCTCCGTGTCTTC 18688
Db 16797 GCTACCTGACACTGTGGAACAGTGTGAGCTGTGCTACGAGAGAGTCTCCGTGTCTTC 16856
QY 18689 CCGCATGCCCCAGACATCGGAGAGACTGTGTGCGGAGAGGTTTCCGCGTTTGCCA 18748
Db 16857 CCGCATGCCCCAGACATCGGAGAGACTGTGTGCGGAGAGGTTTCCGCGTTTGCCA 16916
QY 18749 GCGCACCTGTGGGCGATGGGGAGAACGACGACGTTTCTACGCTTTCACCGCGACA 18808
Db 16917 GCGCACCTGTGGGCGATGGGGAGAACGACGACGTTTCTACGCTTTCACCGCGACA 16976
QY 18809 ACCCACTGGACATAGTACCCCGCTGTGTGAGCGCGCGGATCGGAGCTGTGTGCGG 18868
Db 16977 ACCCACTGGACATAGTACCCCGCTGTGTGAGCGCGCGGATCGGAGCTGTGTGCGG 17036
QY 18869 TTACAGCTCCGCAAAACAGCGGGGTGTGCGGATAGGACTTAAGTATTTGCGGATCG 18928
Db 17037 TTACAGCTCCGCAAAACAGCGGGGTGTGCGGATAGGACTTAAGTATTTGCGGATCG 17096
QY 18929 TTACAGTGTGTGCGCGCGCGGGGTGTCTACCTTCCAAACAGCGGCTTGCAGTC 18988
Db 17097 TTACAGTGTGTGCGCGCGCGGGGTGTCTACCTTCCAAACAGCGGCTTGCAGTC 17156
QY 18989 CCGTGAACAGCGCTGTGACAGCGAGGGGTCTCAAGGCTTAACCTTAAGAGCGTGGATTA 19048
Db 17157 CCGTGAACAGCGCGCTGTGACAGCGAGGGGTCTCAAGGCTTAACCTTAAGAGCGTGGATTA 17216
QY 19049 AAATTCAGAGCTTTCCTGCTATGTACGAGAGCGCGACCCATTTCTTTAACCCAGA 19108
Db 17217 AAATTCAGAGCTTTCCTGCTATGTACGAGAGCGCGACCCATTTCTTTAACCCAGA 17276
QY 19109 AGACCAAGCGCTTTTACCGAGCAAGTTTGTGCGGCTGATATGAGCAACAGCACGCGCA 19168
Db 17277 AGACCAAGCGCTTTTACCGAGCAAGTTTGTGCGGCTGATATGAGCAACAGCACGCGCA 17336
QY 19169 GCGCGGTGAACACCGTCTACGCGGAGAAAGACAGAGGTAGGCTGACCGTCCGCCGCC 19228
Db 17337 GCGCGGTGAACACCGTCTACGCGGAGAAAGACAGAGGTAGGCTGACCGTCCGCCGCC 17396
|||||

QY	20309	ATGATGCGCGGATACACACCCACCCGACAGAGATGAGATGAGTACAGATTAACGAAC	20308
Db	18477	ATGATGCGCGGATACACACCCACCCGACAGAGATGAGATGAGTACAGATTAACGAAC	18356
QY	20369	CAGCGCGTATGTTTAAACCCACTCAGACAGCGGCCCTCGTCTCTGCAAGAGAGGGC	20428
Db	18537	CAGCGCGTATGTTTAAACCCACTCAGACAGCGGCCCTCGTCTCTGCAAGAGAGGGC	18506
QY	20429	CGGTGGCCGGCCCACTGGGGAGAACGTTAATTCCAGCGGCACTCGGGGAGCGCCACG	20488
Db	18597	CGGTGGCCGGCCCACTGGGGAGAACGTTAATTCCAGCGGCACTCGGGGAGCGCCACG	18656
QY	20489	GTAGGCGTGGCCGCCCAACACGACAGTAAACACAGACACAGACAGAGGAACATGACC	20548
Db	18657	GTAGGCGTGGCCGCCCAACACGACAGTAAACACAGACACAGAGGAACATGACC	18716
QY	20549	GGTTAAATTTACTGCTTACAATGGCGGGCGGGCGGGGTCAAGCCAGGTCCATTAAAA	20608
Db	18717	GGTTAAATTTACTGCTTACAATGGCGGGCGGGCGGGGTCAAGCCAGGTCCATTAAAA	18776
QY	20609	CACACCGCGCCCAACCCCAACGCGGGGCGGGCCCTGGAAAGCGGTTCTTCCATG	20668
Db	18777	CACACCGCGCCCAACCCCAACGCGGGGCGGGCCCTGGAAAGCGGTTCTTCCATG	18833
QY	20669	CAAAAGAACCGGCTCACAAAAAGGGCTCGTTTGAACCCATTMTGTCCATCGGTTTCGT	20728
Db	18837	CAAAAGAACCGGCTCACAAAAAGGGCTCGTTTGAACCCATTMTGTCCATCGGTTTCGT	18896
QY	20729	TTTACAGATACGGAAAGCGGCTGTCCTCAAAAACACCCCAAGGGGTTGTCCTAACGGCCAT	20788
Db	18897	TTTACAGATACGGAAAGCGGCTGTCCTCAAAAACACCCCAAGGGGTTGTCCTAACGGCCAT	18956
QY	20789	CTCCATCTATATGAGGGGATGAGGGGTGCTGAGCCCTGAGACTAGATCCGCGCGCTTAA	20848
Db	18957	CTCCATCTATATGAGGGGATGAGGGGTGCTGAGCCCTGAGACTAGATCCGCGCGCTTAA	19016
QY	20849	GTCCTCCAGAGCGGCCACCTTTTCTCAAAATCTTCACGCGCGGAAGGAGCGCGGTCCT	20908
Db	19017	GTCCTCCAGAGCGGCCACCTTTTCTCAAAATCTTCACGCGCGGAAGGAGCGCGGTCCT	19076
QY	20909	CCGACGCTGAAGACAGCAGGGGGATACACGTGTTGTTAAACTGGGGCTCACCCAAAGT	20968
Db	19077	CCGACGCTGAAGACAGCAGGGGGATACACGTGTTGTTAAACTGGGGCTCACCCAAAGT	19136
QY	20969	GTCGACAAAGTCTCCCGGGGTCAGAGGCCCTGAGCGTGAAGCATAGATCGTCAGAGGGC	21028
Db	19137	GTCGACAAAGTCTCCCGGGGTCAGAGGCCCTGAGCGTGAAGCATAGATCGTCAGAGGGC	19196
QY	21029	GTAGCTGGCGATGTTAAACGGGAGCCCGAGGCCCATGTCGGCGGACCTTGTCAGACTG	21088
Db	19197	GTAGCTGGCGATGTTAAACGGGAGCCCGAGGCCCATGTCGGCGGACCTTGTCAGACTG	19256
QY	21089	GCAGGACACGTCTCCCGGAGCCGACGTAAACTGACACAAACTGACACAGGAGGAGAGC	21148
Db	19257	GCAGGACACGTCTCCCGGAGCCGACGTAAACTGACACAAACTGACACAGGAGGAGAGC	19316
QY	21149	CATCGCGGCGAGTGCAGCGGGGTTCCAGCGGCAATTAAGCATCGCGCATCGTGGGGCCG	21208
Db	19317	CATCGCGGCGAGTGCAGCGGGGTTCCAGCGGCAATTAAGCATCGCGCATCGTGGGGCCG	19376
QY	21209	CGTCTTAATTGATTCACACAGTAACACAGCTGGTCACCCCTGACCCCTCGTAGTTGGC	21268
Db	19377	CGTCTTAATTGATTCACACAGTAACACAGCTGGTCACCCCTGACCCCTCGTAGTTGGC	19436
QY	21269	GTCGGCCCCCTGTACTCCGCCCAAAATGTCTCCACTGTGACACCGCTACACGGCCCCAG	21328
Db	19437	GTCGGCCCCCTGTACTCCGCCCAAAATGTCTCCACTGTGACACCGCTACACGGCCCCAG	19496
QY	21329	ATCGCCCTCGGGGCGTCCCGAAAGCCCTGCGCCCAAAAAGCGCGGGA	21379
Db	19497	ATCGCCCTCGGGGCGTCCCGAAAGCCCTGCGCCCAAAAAGCGCGGGA	19547

ORIGIN

Query Match 19.9%; Score 7957; DB 1; Length 10595;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 8257; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 13117 TGTACTGCGCCCCCGGTACGTTGAGTTTCTCAACAGCACACCGCTTTCAAGGC 13176
DB TGTACTGCGCCCCCGGTACGTTGAGTTTCTCAACAGCACACCGCTTTCAAGGC 2146
OY 13177 CAGCTGGGACCCAGAAAGAGATCATCTGACGAGCAACCAAGGTGAGGCGTGCAGAG 13236
DB CAGCTGGGACCCAGAAAGAGATCATCTGACGAGCAACCAAGGTGAGGCGTGCAGAG 2206
OY 13237 ACGTGCGAACACTACTTATAGCGAGCAACGTAACCTACTACTCAAAAGACTAGCTTTC 13296
DB ACGTGCAGAACACTACTTATAGCGAGCAACGTAACCTACTACTCAAAAGACTAGCTTTC 2266
OY 13297 GTGAAAAAATTAACACCTCGAGATATCAACCTCGGTACGTTCAATGCGCCGTGAACCTG 13356
DB GTGAAAAAATTAACACCTCGAGATATCAACCTCGGTACGTTCAATGCGCCGTGAACCTG 2326
OY 13357 TCGTTTATAGAAATATGATTTTCAAGGTCATCGAGCTGTACAGCCGCGGAGAAAAAG 13416
DB TCGTTTATAGAAATATGATTTTCAAGGTCATCGAGCTGTACAGCCGCGGAGAAAAAG 2386
OY 13417 CTGTCCGGGAGCGTTTGTGATATAGAAACCATGTTCAAGGAATCAACTACTACACGCGAA 13476
DB CTGTCCGGGAGCGTTTGTGATATAGAAACCATGTTCAAGGAATCAACTACTACACGCGAA 2446
OY 13477 CGCCTGGCGGAGCTCCGGGAGAGCTGGAGCAACAGATGACCTGAACCGGAGCCGCTG 13536
DB CGCCTGGCGGAGCTCCGGGAGAGCTGGAGCAACAGATGACCTGAACCGGAGCCGCTG 2506
OY 13537 GCCCGGACCTGTCCGAGATATGTCGGGACCTGGGCGCATGTCGCGCGGACGCTGTTAAC 13596
DB GCCCGGACCTGTCCGAGATATGTCGGGACCTGGGCGCATGTCGCGCGGACGCTGTTAAC 2566
OY 13597 GTGGCAGATAGCGATATTAACCTGTTCGATCAATCGAGCGGGTTCTATTAACCTTTATA 13656
DB GTGGCAGATAGCGATATTAACCTGTTCGATCAATCGAGCGGGTTCTATTAACCTTTATA 2626
OY 13657 AAGAGTCCGTTCCGGGCGATGCTCATGATCTGTGATTTGCGGCGTCTGTCGATGTCG 13716
DB AAGAGTCCGTTCCGGGCGATGCTCATGATCTGTGATTTGCGGCGTCTGTCGATGTCG 2686
OY 13717 TTTGCGCTAAACCGGCGGACCAAGCCATCGGCCCGCCCATATCAGATATCTAACCC 13776
DB TTTGCGCTAAACCGGCGGACCAAGCCATCGGCCCGCCCATATCAGATATCTAACCC 2746
OY 13777 GACATAGACAAATATGCAACCGCTGTGGCGGTAAAGTCGACAGAGACAGATTTAAAAACTT 13836
DB GACATAGACAAATATGCAACCGCTGTGGCGGTAAAGTCGACAGAGACAGATTTAAAAACTT 2806
OY 13837 CTCGCCGCGATGCAACAGCTACAGAGAGAGAGCGCTAGGCGTTTAGAGAAACAGCAGAG 13896
DB CTCGCCGCGATGCAACAGCTACAGAGAGAGAGCGCTAGGCGTTTAGAGAAACAGCAGAG 2866
OY 13897 TCAGGCGCCCTGCTTTTCCGGCGGCGGTCAAGCGAGCTAAAAACGTCGCTTTAAGGGGAAT 13956
DB TCAGGCGCCCTGCTTTTCCGGCGGCGGTCAAGCGAGCTAAAAACGTCGCTTTAAGGGGAAT 2926
OY 13957 AAACCGCTGGAAGAGAGAGCTCAAGATATGAATATGAGCAAAATTAACACACCCACAC 14016
DB AAACCGCTGGAAGAGAGAGCTCAAGATATGAATATGAGCAAAATTAACACACCCACAC 2986
OY 14017 GCCTGTACTTCCGCGCGCGAGAGCGCGGCGCAATGATTCGCGACCGCGCGGTCC 14076
DB GCCTGTACTTCCGCGCGCGAGAGCGCGGCGCAATGATTCGCGACCGCGCGGTCC 3046
OY 14077 CCGAGACCTCTAGGCGCGCGGCGGTCTGTATCATATCATGATTTCTTTAAC 14136
DB CCGAGACCTCTAGGCGCGCGGCGGTCTGTATCATATCATGATTTCTTTAAC 3106

OY 14137 CCGTACTGGGCGCTCGCGAGCAAGCCCCCACTCACAGAGGACCGATGCTCCGCC 14196
DB CCGTACTGGGCGCTCGCGAGCAAGCCCCCACTCACAGAGGACCGATGCTCCGCC 3166
OY 14197 CCTGCCGCGCGGACCGCTTACAGCGCGCACACGTTTGTGAGGCTCATCCCGCTGC 14256
DB CCTGCCGCGCGGAGCGGCTTACAGCGCGCACACGTTTGTGAGGCTCATCCCGCTGC 3226
OY 14257 CTCGGAACCGGAGGCGGAGGATGATCCCGGTACAGATCCGTTCCCGCAACGTAC 14316
DB CTCGGAACCGGAGGCGGAGGATGATCCCGGTACAGATCCGTTCCCGCAACGTAC 3286
OY 14317 TTGGAACCGGTGCTCGCGAGAGAGCTGTGCTCCGCAAGAAAGGTTCCATGAGAGCG 14376
DB TTGGAACCGGTGCTCGCGAGAGAGCTGTGCTCCGCAAGAAAGGTTCCATGAGAGCG 3346
OY 14377 CGGACCGCAAGCCCGTCCGCGGACCCCAAGACCAATCCATCAGTTTACGCGTAC 14436
DB CGGACCGCAAGCCCGTCCGCGGACCCCAAGACCAATCCATCAGTTTACGCGTAC 3406
OY 14437 GACGTGTTGAACAACTAGCGGCGGAGAGGTTGCGCGAGTACTTACGCGCTTCCAA 14496
DB GACGTGTTGAACAACTAGCGGCGGAGAGGTTGCGCGAGTACTTACGCGCTTCCAA 3466
OY 14497 ACGGACATTTATCCCAAGCGAACCGTGTCAAGCTCTGCGGCGCAACGAGAGCGCAC 14556
DB ACGGACATTTATCCCAAGCGAACCGTGTCTCAAGCTCTGCGGCGCAACGAGAGCGCAC 3526
OY 14557 AGCGTGTGTAACGTTCCGTCACAGAGTATATTTCTACGCGAAGTTTCCAGCGGC 14616
DB AGCGTGTGTAACGTTCCGTCACAGAGTATATTTCTACGCGAAGTTTCCAGCGGC 3586
OY 14617 ATTAACTACCCCAATCCTCCAGAGGCGCTCAAGAAACAGACCGGCGGCGCGCTGC 14676
DB ATTAACTACCCCAATCCTCCAGAGGCGCTCAAGAAACAGACCGGCGGCGCGCTGC 3646
OY 14677 GCGTTCGAGCAGAAAGAGTGAACAAAGAAATTTCAAAAGAGTACAGCGCGGAGCAT 14736
DB GCGTTCGAGCAGAAAGAGTGAACAAAGAAATTTCAAAAGAGTACAGCGCGGAGCAT 3706
OY 14737 CCGGTACAGGAATACGCTATCGTCGCGTTCCATGCTCTGACACCTCAGGACCGGCTC 14796
DB CCGGTACAGGAATACGCTATCGTCGCGTTCCATGCTCTGACACCTCAGGACCGGCTC 3766
OY 14797 GTCCGTCGCGGCGGAGAGTGTGAGTCAAAACGAGCGCGTCCGCGGCTGCTG 14856
DB GTCCGTCGCGGCGGAGAGTGTGAGTCAAAACGAGCGCGTCCGCGGCTGCTG 3826
OY 14857 GATCAGGCGTTTACACGTTGCGGTGATCTGTCGCGCGCGGCGCACCGCGCTGCGC 14916
DB GATCAGGCGTTTACACGTTGCGGTGATCTGTCGCGCGCGGCGCACCGCGCTGCGC 3886
OY 14917 GCCAGAGTATGCAAGCGGCGCTGGAATGATCTCAACTGGAGAGACCTCAGCTTCAA 14976
DB GCCAGAGTATGCAAGCGGCGCTGGAATGATCTCAACTGGAGAGACCTCAGCTTCAA 3946
OY 14977 GCGAGCGCAGCGAATGCGCGCGCGGACCGGATCGGCGCTTGAATATGAGAGCACTGGA 15036
DB GCGAGCGCAGCGAATGCGCGCGCGGACCGGATCGGCGCTTGAATATGAGAGCACTGGA 4006
OY 15037 GAGGCGGATTTCCGTCGCGCAAGCGCGGAGCGGCGGATCCAGATCTCCGCGCTC 15096
DB GAGGCGGATTTCCGTCGCGCAAGCGCGGAGCGGCGGATCCAGATCTCCGCGCTC 4066
OY 15097 TTCTACAGCACGAGGAAAGCGCGCCCAATCCGCAAAACATATCTTACGCTGGAGAC 15156
DB TTCTACAGCACGAGGAAAGCGCGCGCCCAATCCGCAAAACATATCTTACGCTGGAGAC 4126
OY 15157 TGCAGCCCATTCGCGGACAGCAGAGTTTGGAGTTTCCGTGGGAATATGACATGTCGGG 15216
DB TGCAGCCCATTCGCGGACAGCAGAGTTTGGAGTTTCCGTGGGAATATGACATGTCGGG 4186

QY 15217 TCGTCTTCGCCATGATCCGCGACTTCGAGGTGACTTTTAAACCGGCTATAACATCTCA 15276
DB 4187 TCGTCTTCGCCATGATCCGCGACTTCGAGGTGACTTTTAAACCGGCTATAACATCTCA 4246
QY 15277 AACTTGATCTCCCGTACCTTAATCAGCGAGCTCCGAGGTGATCAACCTTCGATTAAAC 15336
DB 4247 AACTTGATCTCCCGTACCTTAATCAGCGAGCTCCGAGGTGATCAACCTTCGATTAAAC 4306
QY 15337 GAATACACAAAAATAAAAAACCGGCTCATCTTTGAAATTTCACGAGCCCGTGGCGGGGA 15396
DB 4307 GAATACACAAAAATAAAAAACCGGCTCATCTTTGAAATTTCACGAGCCCGTGGCGGGGA 4366
QY 15397 GGGGGGTTCATGAGTGCCTGCTCAAAAAATTAATAGCGGGCATTCGTCCTCATAGACATG 15456
DB 4367 GGGGGGTTCATGAGTGCCTGCTCAAAAAATTAATAGCGGGCATTCGTCCTCATAGACATG 4426
QY 15457 TACACAGTGTGTCGCGCAAAAAGCTCAGCTCTCCGACTACAACTGGACAGCGTGGCGAG 15516
DB 4427 TACACAGTGTGTCGCGCAAAAAGCTCAGCTCTCCGACTACAACTGGACAGCGTGGCGAG 4486
QY 15517 CAGTGTCTGGGTGGAAAAAAGAGAGCATCTGTACAGAGCATTCGCCCTGTGTTCCG 15576
DB 4487 CAGTGTCTGGGTGGAAAAAAGAGAGCATCTGTACAGAGCATTCGCCCTGTGTTCCG 4546
QY 15577 TCAGGTCCGGGGCGGCGGCTAAGTGGGCGAGCTATTGGCTGATGAGACTGGTCCGTG 15636
DB 4547 TCAGGTCCGGGGCGGCGGCTAAGTGGGCGAGCTATTGGCTGATGAGACTGGTCCGTG 4606
QY 15637 ATGAGACTCTTAAATAATGTTTATGATACAGTGGATTTTCGAGATAGCAAGCTGGCC 15696
DB 4607 ATGAGACTCTTAAATAATGTTTATGATACAGTGGATTTTCGAGATAGCAAGCTGGCC 4666
QY 15697 AAGATTACAGGCCAGCGCGCTCTGACGAGAGGCCAAGCTCCGCTGTTCTCTGCTG 15756
DB 4667 AAGATTACAGGCCAGCGCGCTCTGACGAGAGGCCAAGCTCCGCTGTTCTCTGCTG 4726
QY 15757 CTGGAGGCGCGGCGGCGGAGAACTTATCTCCGCTTCCAAAGCGCCGAGGAGACAGGG 15816
DB 4727 CTGGAGGCGCGGCGGCGGAGAACTTATCTCCGCTTCCAAAGCGCCGAGGAGACAGGG 4786
QY 15817 GGCATTACAGGGCGCAGCGTGAATCAACCCCATTCGGGGTATTACAGCAGCGCGTCTG 15876
DB 4787 GGCATTACAGGGCGCAGCGTGAATCAACCCCATTCGGGGTATTACAGCAGCGCGTCTG 4846
QY 15877 GTGCTGATTTTTCAGCCTGTACCCGAGCATTCACAGCGCACAACCTGTGCTACTCC 15936
DB 4847 GTGCTGATTTTTCAGCCTGTACCCGAGCATTCACAGCGCACAACCTGTGCTACTCC 4906
QY 15937 ACCATGATACAGGAGAGAACCTGCACTCGACCCCAACCTGACGCGCGGAGCATACGAG 15996
DB 4907 ACCATGATACAGGAGAGAACCTGCACTCGACCCCAACCTGACGCGCGGAGCATACGAG 4966
QY 15997 ACGTTCGTGCTAGAGCGCGGAGCGGTACATTTTGTAAAAAACAAGGGGAGTCTG 16056
DB 4967 ACGTTCGTGCTAGAGCGCGGAGCGGTACATTTTGTAAAAAACAAGGGGAGTCTG 5026
QY 16057 CTGGGAAGACTCTAAACGTGTGTGTTAGAAAAAGCGAAGGGCGATCCGGCGCAACCTG 16116
DB 5027 CTGGGAAGACTCTAAACGTGTGTGTTAGAAAAAGCGAAGGGCGATCCGGCGCAACCTG 5086
QY 16117 GGGTGGATGAGACCCGCTGCTAAAAACACTTATAGATAAACACAGCTGGCCATCAAGGTG 16176
DB 5087 GGGTGGATGAGACCCGCTGCTAAAAACACTTATAGATAAACACAGCTGGCCATCAAGGTG 5146
QY 16177 ACATGTAAAGCGGTTTACGGGTTCACCGGGGTGGCGAGCGGCTCTCCATGCAATTAAC 16236
DB 5147 ACATGTAAAGCGGTTTACGGGTTCACCGGGGTGGCGAGCGGCTCTCCATGCAATTAAC 5206
QY 16237 ATAAGCGAAACCGTGAAGCTTCGCGGGGCGCACGATGCTGAGATGTCAAAAGTCTTAAC 16296
DB 5207 ATAAGCGAAACCGTGAAGCTTCGCGGGGCGCACGATGCTGAGATGTCAAAAGTCTTAAC 5266
QY 16297 GAGGCGCTGACGAGAGAACTGCGAAGCGGTCTCGGTGCGAGGTGACCGCCGCTCAC 16356

DB 5267 GAGGCGCTGACGAGAGAACTGCGAAGCCGTCTGGTTCGAGGTGACCGCCGCTCAC 5326
QY 16357 GGGCGCGGTTTGGCTGCTGCTACAGGTGACACGAGCTCCCTTTATACGGCTCGAGGT 16416
DB 5327 GGGCGCGGTTTGGCTGCTGCTACAGGTGACACGAGCTCCCTTTATACGGCTCGAGGT 5386
QY 16417 TATTCCGGGAAGCCGTTTCCGCTTCTGTGACGATCTGGCGCCAGAGTCACTGCGGAC 16476
DB 5387 TATTCCGGGAAGCCGTTTCCGCTTCTGTGACGATCTGGCGCCAGAGTCACTGCGGAC 5446
QY 16477 CTGTCGCCCGCAACCTTAAGCTAAGCGCGGAATAACGTTCAAGTGTCTGCTGCTG 16536
DB 5447 CTGTCGCCCGCAACCTTAAGCTAAGCGCGGAATAACGTTCAAGTGTCTGCTGCTG 5506
QY 16537 ACGAAAAAGCGCTACATCGGGGTCTCAATTGAAACGAAAAATGCTCATGAAAGGGTGCAG 16596
DB 5507 ACGAAAAAGCGCTACATCGGGGTCTCAATTGAAACGAAAAATGCTCATGAAAGGGTGCAG 5566
QY 16597 CTCATTGCGAAAAAGCGCTGCAAGTTTGTCAAGAGCATGCGCGCATCTGAGACTG 16656
DB 5567 CTCATTGCGAAAAAGCGCTGCAAGTTTGTCAAGAGCATGCGCGCATCTGAGACTG 5626
QY 16657 GTGCTCCAGATTCGAGGTCAAGGCTCGCGGGCGGCTGTTGTGCAAGCGCGCGCGCAC 16716
DB 5627 GTGCTCCAGATTCGAGGTCAAGGCTCGCGGGCGGCTGTTGTGCAAGCGCGCGCGCAC 5686
QY 16717 GCGGTATACGAGGAGGGGCTGCCGCTGGCTTATTAATAATCTAGAGTCTCAACGCG 16776
DB 5687 GCGGTATACGAGGAGGGGCTGCCGCTGGCTTATTAATAATCTAGAGTCTCAACGCG 5746
QY 16777 AGCTATCTGAGCTCCGAAACAGCGTGTGCCCATGAGACATTAACGTTTCCACCGAG 16836
DB 5747 AGCTATCTGAGCTCCGAAACAGCGTGTGCCCATGAGACATTAACGTTTCCACCGAG 5806
QY 16837 CTCAGCGCGCGCTGCGGATTAAGACCAACCACTGCGCCACCTGGGGGTGTACCA 16896
DB 5807 CTCAGCGCGCGCTGCGGATTAAGACCAACCACTGCGCCACCTGGGGGTGTACCA 5866
QY 16897 AAGCTGGCGAGCAGGTGCGAGAGCTGCCCAAGTGCAGATAGAAATCCCTACGTGTT 16956
DB 5867 AAGCTGGCGAGCAGGTGCGAGAGCTGCCCAAGTGCAGATAGAAATCCCTACGTGTT 5926
QY 16957 GTTGACGCGCGCGGTCTCTAAAGTGCAGCTGTGCCGAACCCGGAATTAAGTCAACAG 17016
DB 5927 GTTGACGCGCGCGGTCTCTAAAGTGCAGCTGTGCCGAACCCGGAATTAAGTCAACAG 5986
QY 17017 CACCAATTCGCGTGGCGGTGCACTAATTTGCAAACTGCTGACGGCGGCGCAAC 17076
DB 5987 CACCAATTCGCGTGGCGGTGCACTAATTTGCAAACTGCTGACGGCGGCGCAAC 6046
QY 17077 ATCTTCAGTGTCTGTTCGGCAACAACGCGGAGACACGAGTGGCCATCTCTACAAATTT 17136
DB 6047 ATCTTCAGTGTCTGTTCGGCAACAACGCGGAGACACGAGTGGCCATCTCTACAAATTT 6106
QY 17137 CTCACGTCGCCGTATTAAGCTGTTCTGTGACGCCAATTGGAGACGCCAACAATAAGAC 17196
DB 6107 CTCACGTCGCCGTATTAAGCTGTTCTGTGACGCCAATTGGAGAACGCCAACAATAAGAC 6166
QY 17197 CCGCGCAGCGAGATCCGAGGAGAGCTGAGCGGCGGAGGCGCAACGAGAGACCGC 17256
DB 6167 CCGCGCAGCGAGATCCGAGGAGAGCTGAGCGGCGGAGGCGCAACGAGAGACCGC 6226
QY 17257 CACCATGCTGTGTTAAAGCACTGTGCTGCTCGCGCACTGGAGAGTACTTTTACCG 17316
DB 6227 CACCATGCTGTGTTAAAGCACTGTGCTGCTCGCGCACTGGAGAGTACTTTTACCG 6286
QY 17317 GGGTAGATTACGCTTGTCAACTCAACCGCTGCAACGTTCAAGGCCACGCGGGCTA 17376
DB 6287 GGGTAGATTACGCTTGTCAACTCAACCGCTGCAACGTTCAAGGCCACGCGGGCTA 6346
QY 17377 GCGCAGGCTGCACTCCCTTCTCGCTGCAACGAGTACTGCAACCAATTTGGCGTTGCG 17436

Db 6347 CGCAGGGTCCGACCTCCCTTCTGCTCGACAGTTACTCCACCACATTTTCGCTTCCG 6406
QY 17437 ACTGTGACGGGTCTCAAGAACTGCCCCCTTCCTCGAGTGGCGGCTTATCGGCC 17496
Db 6407 ACTGTGACGGGTCTCAAGAACTGCCCCCTTCTCCAGTGGCGGCTTATCGGCC 6466
QY 17497 GTTGGATTCCGCGCGGACGCGGAGCGCGCGCTGGCCCCCGGGTTCGTGTGGATC 17556
Db 6467 GTTGGATTCCGCGCGGACGCGGAGCGCGGCGCTGGCCCCCGGGTTCGTGTGGATC 6526
QY 17557 CTTCGCCCCGTGACCGTGTGGTTAAACGAGCGGGCGGACACGATCCGGTTCGCT 17616
Db 6527 CTTCGCCCCGTGACCGTGTGGTTAAACGAGCGGGCGGACACGATCCGGTTCGCT 6586
QY 17617 CCTCTTCTAAGCGGATGACCTGGAGCGCGGCTGACGTCAGTCCTTCCGCGAAGAGG 17676
Db 6587 CCTCTTCTAAGCGGATGACCTGGAGCGCGGCTGACGTCAGTCCTTCCGCGAAGAGG 6646
QY 17677 CGGCGCGGCTCGGAGGCGACCCCAAGCCACCTGCGCGACCGAAGCCTGCGCGTGG 17736
Db 6647 CGGCGCGGCTCGGAGGCGACCCCAAGCCACCTGCGCGAGACCGAAGCCTGCGCGTGG 6706
QY 17737 ACCCTGCGGCTCTCCGCGAGGGCTCTCAGACGTGCCCCATTCCTTCTGTTGCGTATT 17796
Db 6707 ACCCTGCGGCTCTCCGCGAGGGCTCTCAGACGTGCCCCATTCCTTCTGTTGCGTATT 6766
QY 17797 TCCACGGGCAACTGGGTGGCTGCTAAGCTGTGGGTTACAGGTGAGGCGGCTTTC 17856
Db 6767 TCCACGGGCAACTGGGTGGCTGCTAAGCTGTGGGTTACAGGTGAGGCGGCTTTC 6826
QY 17857 GGATGACGCGGCGCACAGGAGCGCGGATCTCCCGCAAAATACGTACAGTTAGTACTC 17916
Db 6827 GGATGACGCGGCGCACAGGAGCGCGGATCTCCCGCAAAATACGTACAGTTAGTACTC 6886
QY 17917 CGGCGGTAACTCTGCAAGGGCTCCGTTACACAGCTGTCCCGTGGCGGTGTAACAGGC 17976
Db 6887 CGGCGGTAACTCTGCAAGGGCTCCGTTACACAGCTGTCCCGTGGCGGTGTAACAGGC 6946
QY 17977 GCAAAATGAAATCATCTACGCTCCCGGGGACCCCAAGCCGAGATAGTCTGGGCGACTC 18036
Db 6947 GCAAAATGAAATCATCTACGCTCCCGGGGACCCCAAGCCGAGATAGTCTGGGCGACTC 7006
QY 18037 CGGACCCGCTCTGCCACCAACACCGGCGCGCTATTGGGGGTCTACGCCGACGCCGA 18096
Db 7007 CGGACCCGCTCTGCCACCAACACCGGCGCGCTATTGGGGGTCTACGCCGACGCCGA 7066
QY 18097 AAAAAACATCCAACTGGAAGCTCCGCGGAAGTCCGGGTTCAAGTTAACTTCCAAACAGG 18156
Db 7067 AAAAAACATCCAACTGGAAGCTCCGCGGAAGTCCGGGTTCAAGTTAACTTCCAAACAGG 7126
QY 18157 AGCGGCGCTGGGGGCGATCTGGGCTTCTGTGTCAGGGGCGTGGGACCGGAGCCCTATT 18216
Db 7127 AGCGGCGCTGGGGGCGATCTGGGCTTCTGTGTCAGGGGCGTGGGACCGGAGCCCTATT 7186
QY 18217 GGTGCTCAACCCCGGACCTTGTCTTCCGTTGCAACCAACCTGCGGCTATTCAACCC 18276
Db 7187 GGTGCTCAACCCCGGACCTTGTCTTCCGTTGCAACCAACCTGCGGCTATTCAACCC 7246
QY 18277 CAAGGTACCCCGCAAGACTATTAAGAGACACCTTGTGGCGCGCGCGGCTTCCGCC 18336
Db 7247 CAAGGTACCCCGCAAGACTATTAAGAGAGACACCTTGTGGCGCGCGCGGCTTCCGCC 7306
QY 18337 GGTGTTGGGATTAACTCCGCGGAGACGCGCGCGGAGACCTGTCGGGTCAACGAGAC 18396
Db 7307 GGTGTTGGGATTAACTCCGCGGAGACGCGCGCGGAGACCTGTCGGGTCAACGAGAC 7366
QY 18397 CGGGGCGCTCTTCATTAACGGGTTCACAATCCGGTGTTCACAGGGGTGCTCGGC 18456
Db 7367 CGGGGCGCTCTTCATTAACGGGTTCACAATCCGGTGTTCACAGGGGTGCTCGGC 7426
QY 18457 GAGGTGTACAGTGTCCCTACGCGACACGAGGGGTCCAGCAAGCATGAACATTCAGCGCA 18516
Db 7427 GAGGTGTACAGTGTCCCTACGCGACACGAGGGGTCCAGCAAGCATGAACATTCAGCGCA 7486

QY 18517 ACGATGGGAACACCGGTGCTGTTCTTTCGGCGAGTGGGACACTCGAGTCTAGTGGAC 18576
Db 7487 ACGATGGGAACACCGGTGCTGTTCTTTCGGCGAGTGGGACACTCGAGTCTAGTGGAC 7546
QY 18577 AACGGCACGCGGTACAGCTCCCTGGTGTGGCGGCGCAATATTACAGAGGCTACCTG 18636
Db 7547 AACGGCACGCGGTACAGCTCCCTGGTGTGGCGGCGCAATATTACAGAGGCTACCTG 7606
QY 18637 ACATGTGTGAACAGTCAAGAGTGTGCTCACGGAAGAGTCTCCGTGTCTCGCGCATTC 18696
Db 7607 ACATGTGTGAACAGTCAAGAGTGTGCTCACGGAAGAGTCTCCGTGTCTCGCGCATTC 7666
QY 18697 CCCAGCATCGGGAAGCTGGTGGGAAGAGTTTCCCGGCTTCCGCTTTCGCGAGCGCACT 18756
Db 7667 CCCAGCATCGGGAAGCTGGTGGGAAGAGTTTCCCGGCTTCCGCTTTCGCGAGCGCACT 7726
QY 18757 CTGGCGATCGGGGAACACGACCGTGTCTACGCGTTCCGTTACCGCGACACCCACTG 18816
Db 7727 CTGGCGATCGGGGAACACGACCGTGTCTACGCGTTCCGTTACCGCGACACCCACTG 7786
QY 18817 GACATAGTACCCCGCTGTGAGCGCGCGGATGCGGAGCTGTGCTCGGGTTACGCT 18876
Db 7787 GACATAGTACCCCGCTGTGAGCGCGCGGATGCGGAGCTGTGCTCGGGTTACGCT 7846
QY 18877 CCGCAACACGCGGGGTGTCGATACGAGCTTAAGTATTTCGGTGGCATGTTACGGTG 18936
Db 7847 CCGCAACACGCGGGGTGTCGATACGAGCTTAAGTATTTCGGTGGCATGTTACGGTG 7906
QY 18937 GTGGCGCCGCGGGGGTTCCTACACTTTCACAAAGACGCGTTCCGATCGCGTGACA 18996
Db 7907 GTGGCGCCGCGGGGGTTCCTACACTTTCACAAAGACGCGTTCCGATCGCGTGACA 7966
QY 18997 GACGCGTACCCAGGAGGCTCCAGGCTAACCTCTGAAGAGCGTGGATTAATAATTCAA 19056
Db 7967 GACGCGTACCCAGGAGGCTCCAGGCTAACCTCTGAAGAGCGTGGATTAATAATTCAA 8026
QY 19057 GGCCTTCCCGTCTTCTGACAGAGACCGCGACCCATTCCTTAAACCAGAACACAG 19116
Db 8027 GGCCTTCCCGTCTTCTGACAGAGACCGCGACCCATTCCTTAAACCAGAACACAG 8086
QY 19117 CCCTTACCGAGCAAGATTTTCCGCTGATCATGACAAACGACGCGCGCGCTC 19176
Db 8087 CCCTTACCGAGCAAGATTTTCCGCTGATCATGACAAACGACGCGCGCGCTC 8146
QY 19177 AACACCGTACTCTGGAACACGACGCTGAGGGTGAACCGGACCCCGCGGAACA 19236
Db 8147 AACACCGTACTCTGGAACACGACGCTGAGGGTGAACCGGACCCCGCGGAACA 8206
QY 19237 ATCGTACCGAGCGCGCGGTGACGCGGACCGCTGCTCACCGGTAAATGCGCAATCGCC 19296
Db 8207 ATCGTACCGAGCGCGCGGTGACGCGGACCGCTGCTCACCGGTAAATGCGCAATCGCC 8266
QY 19297 TTTGCGCAACCCATTACTTGAACCTCCGTGTGTCACCAAGCGGCAATTCACGCC 19356
Db 8267 TTTGCGCAACCCATTACTTGAACCTCCGTGTGTCACCAAGCGGCAATTCACGCC 8326
QY 19357 GTGGGTACAGTGGGCTGACCGGTGACATCCCAACTGTAAGAAATTTGTAAGTAC 19416
Db 8327 GTGGGTACAGTGGGCTGACCGGTGACATCCCAACTGTAAGAAATTTGTAAGTAC 8386
QY 19417 GGTAAACACTAGTCTCGGCAATTTAAACGCAAGTGAAGGGGATTAATAGCAATACGCC 19476
Db 8387 GGTAAACACTAGTCTCGGCAATTTAAACGCAAGTGAAGGGGATTAATAGCAATACGCC 8446
QY 19477 CACAACGCGGGTTCGGAATTCAGAGTTCGAGTGGCCACGAAACGCGGAGATTGAAGTT 19536
Db 8447 CACAACGCGGGTTCGGAATTCAGAGTTCGAGTGGCCACGAAACGCGGAGATTGAAGTT 8506
QY 19537 TTGTTAAACACAGTGTCCAGGCGCGCGGTATCATACACCGGAGACGACGTGGGGCA 19596
Db 8507 TTGTTAAACACAGTGTCCAGGCGCGCGGTATCATACACCGGAGACGACGTGGGGCA 8566

QY	19397	GCCATCTTCGTGTTCCGCGCGCGGTTGGTGGCCCGGCGAATCGCGCAGCTCCTCGGC	19536
Db	8567	GCCATCTTCGTGTTCCGCGCGCGGTTGGTGGCCCGGCGAATCGCGCAGCTCCTCGGC	8626
QY	19657	CACGATCGCGCGCGCTGGAGCTGCGCGGGGGGGTACAGTGGACAGCCAAACCTGT	19716
Db	8627	CACGATCGCGCGCGCTGGAGCTGCGCGGGGGGGTACAGTGGACAGCCAAACCTGT	8686
QY	19717	AGTTTGAAGACATGATACCTGTTTTCCACGTAATTAATTAATTAACCTGTTGCTGTATC	19776
Db	8687	AGTTTGAAGACATGATACCTGTTTTCCACGTAATTAATTAATTAACCTGTTGCTGTATC	8746
QY	19777	GCTACACAAAGCCAAACCGTCTCTCATCTCGGGGTGCGCGGCTCGGAAACACAAAG	19836
Db	8747	GCTACACAAAGCCAAACCGTCTCTCATCTCGGGGTGCGCGGCTCGGAAACACAAAG	8806
QY	19837	GTCGCTCAAAACACCCCGCTCCGAGACCCCTGGCCACAAACAGTAACGGCTTCGTT	19896
Db	8807	GTCGCTCAAAACACCCCGCTCCGAGACCCCTGGCCACAAACAGTAACGGCTTCGTT	8866
QY	19897	AGATGAGTTTATTTATTTATTTATTAATCATCATAGCTATTTGGCGCGCGCTCCGCA	19956
Db	8867	AGATGAGTTTATTTATTTATTTATTAATCATCATAGCTATTTGGCGCGCGCTCCGCA	8926
QY	19957	AAACATCTGTAGATATTCCAGTATGCGAAACGCGTGAACAACGTCCTCGGGGCGCTG	20016
Db	8927	AAACATCTGTAGATATTCCAGTATGCGAAACGCGTGAACAACGTCCTCGGGGCGCTG	8986
QY	20017	CCCTCCCAAGCGACGCGGTTTTTTCATTAAGACTCGGGCCACCACTCTGTTTATTAAC	20076
Db	8987	CCCTCCCAAGCGACGCGGTTTTTTCATTAAGACTCGGGCCACCACTCTGTTTATTAAC	9046
QY	20077	GGGAAGCTCTCAATTAAGAGTGCAGAGGCGGACACACACGCTACCGCGGACCAAT	20136
Db	9047	GGGAAGCTCTCAATTAAGAGTGCAGAGGCGGACACACACGCTACCGCGGACCAAT	9106
QY	20137	GGCGCGGCGTCGCGCTCCCGGGCGGTCGTCACAGACATCTTCAGTGGCTCAGGTA	20196
Db	9107	GGCGCGGCGTCGCGCTCCCGGGCGGTCGTCACAGACATCTTCAGTGGCTCAGGTA	9166
QY	20197	ACCTCTGTAGGCGCGGAGCGCGGAACATAGGCGTTCATACACTCGGGCCCGGGAACCTC	20256
Db	9167	ACCTCTGTAGGCGCGGAGCGCGGAACATAGGCGTTCATACACTCGGGCCCGGGAACCTC	9226
QY	20257	GGCGCGCTGGCACTCAACGTTTACACATCAATATAGGGAAGTGAACAAAGCATATGCG	20316
Db	9227	GGCGCGCTGGCACTCAACGTTTACACATCAATATAGGGAAGTGAACAAAGCATATGCG	9286
QY	20317	CGGCTACTCAACGACCCGACAGAGAGTGGATGTGTGGCAACAGTAAACGACACGCGTG	20376
Db	9287	CGGCTACTCAACGACCCGACAGAGAGTGGATGTGTGGCAACAGTAAACGACACGCGTG	9346
QY	20377	TATGTTTAACCCCACTTCAAGACAGGCGCCCGTGTCGTAAGAAGAGCGCGGTTGCC	20436
Db	9347	TATGTTTAACCCCACTTCAAGACAGGCGCCCGTGTCGTAAGAAGAGCGCGGTTGCC	9406
QY	20437	GGCCCACTGGGGGGAACGTTTAATTCACGCGGACGTGCGGGGAGCGCCAGGCTAGGCT	20496
Db	9407	GGCCCACTGGGGGGAACGTTTAATTCACGCGGACGTGCGGGGAGCGCCAGGCTAGGCT	9466
QY	20497	GGCCGCCCAACACGACAGGTAATAAACAAGACGAAACGACAGAGGGAACATGACCGTTAAT	20556
Db	9467	GGCCGCCCAACACGACAGGTAATAAACAAGACGAAACGACAGAGGGAACATGACCGTTAAT	9526
QY	20557	TACTCGCTTACATTCGCGGGCGCGCGCGGTCAACGCCAGGTGTCATTTAAAAACAACGG	20616
Db	9527	TACTCGCTTACATTCGCGGGCGCGCGCGGTCAACGCCAGGTGTCATTTAAAAACAACGG	9586
QY	20617	CCGCGCAACCCCAAGCGGGGCGCGCGCTGGAACCGGTTCTTCCTTCCATTCGCAAGAAG	20676
Db	9587	CCGCGCAACCCCAAGCGGGGCGCGCGCTGGAACCGGTTCTTCCTTCCATTCGCAAGAAG	9646
QY	20677	CGGCTCACAAAAAGGCTGCTTTTGAACCATTTGTGCATCGGGGTTTCGTTTCAAT	20736

Db	Accession	Source	Organism	Reference	Authors	Title
Db	9647	CGCGGACAA	AAAGGGCGTGTGGAAACCCATTTTGGCCATTCGGGGTTTGGTTTCAGAT	9706		
QY	20737	ACGGAAGGCGTGC	TCGCAAAACACCCAAACGGGGGTGTCGTCAAACGGCCATCTCCATCT	2079		
Db	9707	ACGGAACGCGTCT	CGTCCAAACACCCACACGGGGGTGTGCTCAACGGCCATCTCCATCT	9766		
QY	20797	CTATGTGGGATG	GGGGTGTGAGCCCTCGACATCCAGATCCGCGCGGCTAAAGTCGCA	2085		
Db	9767	CTATGTGGGATG	GGGGGTGTGAGCCCTCGACATCCAGATCCGCGCGGCTAAAGTCGCA	9826		
QY	20857	GACGCGCCACCT	TTCTCAAAATCTTCAGCCCGGAAACGACGCGGGGTCTCTCCGACGT	2091		
Db	9827	GACGCGCCACCT	TTCTCAAAATCTTCAGCCCGGAAACGACGCGGGGTCTCTCCGACGT	9886		
QY	20917	GAAGCAGCAGG	GGGATCAACGCTGTTGTTGTTAAAGTGGGGCTCAACCAAGGTGACAA	2097		
Db	9887	GAAGCAGCAGG	GGGATCAACGCTGTTGTTGTTAAAGTGGGGCTCAACCAAGGTGACAA	9946		
QY	20977	AGTCTCCCGGG	GTGAGGCCGTGACGTCAGATCAGATCAGTACGAGAGGGCGTAGCTGG	2103		
Db	9947	AGTCTCCCGGG	GTGAGGCCGTGACGTCAGATCAGATCAGTACGAGAGGGCGTAGCTGG	1000		
QY	21037	CGATGTTAAAC	CGGACCCGACATGTGTGCGGACCTTGTTAAAGCTGGCAGAGCA	2109		
Db	10007	CGATGTTAAAC	CGGACCCGACATGTGTGCGGACCTTGTTAAAGCTGGCAGAGCA	1006		
QY	21097	GCTCCCCCGGC	ACGTAACCTGACACAAACGCTGACAGAGAGGAGAGCCATCCGCG	2115		
Db	10067	GCTCCCCCGGC	ACGTAACCTGACACAAACGCTGACAGAGAGGAGAGCCATCCGCG	1012		
QY	21157	CGAGGTCGCG	GGGGTCCACGCGACATTAACGATCGCGCGATGTGGGGCGCGCTGTAA	2121		
Db	10127	CGAGGTCGCG	GGGGTCCACGCGACATTAACGATCGCGCGATGTGGGGCGCGCTGTAA	1018		
QY	21217	TTAAGTCACAC	GCTAACGACGCTGTGCACCCCTTAACCTGCTAAGTTGGCGTGGCCC	2127		
Db	10187	TTAAGTCACAC	GCTAACGACGCTGTGCACCCCTTAACCTGCTAAGTTGGCGTGGCCC	1024		
QY	21277	CCCGTACTCGC	CGCCCAAAATGTCTCCACTGTGAACCCGTCACCGGCCCCACGATCGCCT	2133		
Db	10247	CCCGTACTCGC	CGCCCAAAATGTCTCCACTGTGAACCCGTCACCGGCCCCACGATCGCCT	1030		
QY	21337	CGCGGCGGTC	CCCGAGCCCTGCGCGCCCAAAAGGCGCGGGA	21379		
Db	10307	CGCGGCGGTC	CCCGAGCCCTGCGCGCCCAAAAGGCGCGGGA	10349		
RESULT 4	AF087411	3804 bp	DNA	linear	VRL 04-NOV-1999	
LOCUS	AF087411	Rhesus macaque rhadinovirus R2 protein, thymidylate synthase, and				
DEFINITION	AF087411.1	R3 protein genes, complete cds.				
ACCESSION	AF087411					
KEYWORDS	AF087411.1	GI:5823013				
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
AUTHORS						
REFERENCE						
AUTHORS						
TITLE						

OY	20903	GGTCTCCGACGCTGGAAGCAGCAGGAGATCAAGCTGTTTGTGTAACGTGGCGTCAC	20962
Db	1501	GGCTCTCCGACGCTGGAAGCAGCAGGAGATCAAGCTGTTTGTGTAACGTGGCGTCAC	1560
OY	20963	CAAGGTGACCAAAAGCTCCCGGGGTCCAGGCCGTGACGTGAGCGTCAAGATAGCTCAG	21022
Db	1561	CAAGGTGACCAAAAGCTCCCGGGGTCCAGGCCGTGACGTGAGCGTCAAGATAGCTCAG	1620
OY	21023	GAGGCGGTAGCTGCGATGTTTAAACGGGACCCGAGGACCCATGTCGGCGACCTCTGTA	21082
Db	1621	GAGGCGGTAGCTGCGATGTTTAAACGGGACCCGAGGACCCATGTCGGCGACCTCTGTA	1680
OY	21083	CAGCTGCGAGACAGCTCTCCCGGAGCCAGCTAAACTGACACAAAAGTGCACAGAGAG	21142
Db	1681	CAGTGTGCAGAGACAGCTCTCCCGGAGCCAGCTAAACTGACACAAAAGTGCACAGAGAG	1740
OY	21143	GAGAGCCATCCGCGAGGTCCGGGGGTCCACGGGCACATTAAGCATGGCGCATCGTG	21202
Db	1741	GAGAGCCATCCGCGCGAGGTCCGGGGGTCCACGGGCACATTAAGCATGGCGCATCGTG	1800
OY	21203	GGGCGGCTGTTAATTAGATCCACACAGTAACGACAGTGTGTCACCCCTGACCCCTGTA	21262
Db	1801	GGGCGGCTGTTAATTAGATCCACACAGTAACGACAGTGTGTCACCCCTGACCCCTGTA	1860
OY	21263	GTTGGCGTGGGCCCCCTGTACTTCGCCCCCAAAATGTCTCACTGGAACCGTGCACGG	21322
Db	1861	GTTGGCGTGGGCCCCCTGTACTTCGCCCCCAAAATGTCTCACTGGAACCGTGCACGG	1920
OY	21323	CCCCAGATGCGCCTCGGGGGGGTCCCGAAGCCCTGCGCGCCCAAAAAGGCGGGACCC	21382
Db	1921	CCCCAGATGCGCCTCGGGGGGGTCCCGAAGCCCTGCGCGCCCAAAAAGGCGGGACCC	1980
OY	21383	GTGCGCGTCCCAATTTTATAGCCGCGGCGCGACGACGTGCTGGAGATCGGTGAGCCCT	21442
Db	1981	GTGCGCGTCCCAATTTTATAGCCGCGGCGCGACGACGTGCTGGAGATCGGTGAGCCCT	2040
OY	21443	GATTAACCAACGACACTCTCTCCACGACGCCCTTCGAAAAACCCCTTTGGTGTTAACG	21502
Db	2041	GATTAACCAACGACACTCTCTCCACGACGCCCTTCGAAAAACCCCTTTGGTGTTAACG	2100
OY	21503	AGGAACCTCGCCCTGAGTTATATGAGGGCTGAACCCGACACGAGACTGGTGCCAC	21562
Db	2101	AGGAACCTCGCTCTGAGTTATATGAGGGCTGAACCCGACACGAGACTGGTGCCAC	2160
OY	21563	GCCCCCTCTCTCCCTCCCTGACAGCGCGTGTATTAATTAATTCAGGTGCGCAAGTA	21622
Db	2161	GCCCCCTCTCTCCCTCCCTGACAGCGCGTGTATTAATTAATTAATTCAGGTGCGCAAGTA	2220
OY	21623	CTGAGACTCGCCTGGTGTCCGCGGCGACGCGACGCGGACGCGCGCGGCACTTCCGGTCC	21682
Db	2221	CTGAGACTCGCCTGGTGTCCGCGGCGACGCGGACGCGGACGCGCGCGGCACTTCCGGTCC	2280
OY	21683	GGAAAAAACCCCGAGTGTGCGGCGCGGATTCACGCAAGCGGATATATTTTTTT	21742
Db	2281	GGAAAAAACCCCGAGTGTGCGGCGCGGATTCACGCAAGCGGATATATTTTTTT	2340
OY	21743	AACGTACAGATACCGAGATGACACAGACAATCATATTTACAAACGAGAGTCTTTACAA	21802
Db	2341	AACGTACAGATACCGAGATGACACAGACAATCATATTTACAAACGAGAGTCTTTACAA	2400
OY	21803	CTATTAACCGTAAACGGCTGAAGACGAATCTTATTTTAAAGGACCTTGGCGGGCCGAC	21862
Db	2401	CTATTAACCGTAAACGGCTGAAGACGAATCTTATTTTAAAGGACCTTGGCGGGCCGAC	2460
OY	21863	CACAGGGGCGGCCCGGTGTGTACGAGTAAATAACCCAGCTGTCTCCCAAGCGCTTCC	21922
Db	2461	CACAGGGGCGGCCCGGTGTGTACGAGTAAATAACCCAGCTGTCTCCCAAGCGCTTCC	2520
OY	21923	CCGAGCGTGAAGCTGTCCCAAAAGCCAAACACACAGATATTAATTAATTAATTAACATG	21982
Db	2521	CCGAGCGTGAAGCTGTCCCAAAAGCCAAACACACAGATATTAATTAATTAATTAACATG	2580
OY	21983	TTTATTTTATTAACCTTAACGCGCATTAATGCTTCTTAACGAGGGCCATGAAGCAAC	22042

Db	2581	TTTTATTTTTTTATAAACTTAACGGCCGATTAAGCTTTCTTAACAGGGGCAATTAACAACAC	2640
OY	22043	GTGGCAGGCGGCAATTCGGCGCCTCAAAAAGCAACGCACAACCGGGCGCTGTAAACACGTA	22102
Db	2641	GTGGCAGGCGGCAATTCGGCGCCTCAAAAAGCAACGCACAACCGGGCGCTGTAAACACGTA	2700
OY	22103	AACAACAACATATTAGCCATTGTAACCGTAATAATCCCAACCCCTGTGCTCCGAGGCATT	22162
Db	2701	AACAACAACATATTAGCCATTGTAACCGTAATAATCCCAACCCCTGTGCTCCGAGGCATT	2760
OY	22163	CGCCACAGCTGGGCTCTACGTCGAGGGGTGTTCTAAGTCGCAATTTTGAGCCCTTGGCACGGC	22222
Db	2761	CGCCACAGCTGGGCTCTACGTCGAGGGGTGTTCTAAGTCGCAATTTTGAGCCCTTGGCACGGC	2820
OY	22223	GCGCTCGCTTAATGTAATGGTTCTTAATTCGCGCTCAAGGCGCAAGGCGCTCTGGAATCGTCAA	22283
Db	2821	GCGCTCGCTTAATGTAATGGTTCTTAATTCGCGCTCAAGGCGCAAGGCGCTCTTGGGAATCGTCAA	2880
OY	22283	TCAGGCTCGGCGGGGTCTTCTGCCCCTTTTGGAGCGCTGTCCACCGCCTGAAGCAGTT	22342
Db	2881	TCAGGCTCGGCGGGGTCTTCTGCCCCTTTTGGAGCGCTGTCCACCGCCTGAAGCAGTT	2940
OY	22343	TCTTACATGCGTCTGTCCTCCCGGGATTTGGCACACAGCTTTTACCGGGCGGAGTGTAAATA	22402
Db	2941	TCTTACATGCGTCTGTCCTCCCGGGATTTGGCACACAGCTTTTACCGGGCGGAGTGTAAATA	3000
OY	22403	TCACGCGCTCCACCGAGACATGCGACAGAGGTGTGGAGTAAAGACACTAAACCGGGGTG	22462
Db	3001	TCACGCGCTCCACCGAGACATGCGACAGAGGTGTGGAGTAAAGACACTAAACCGGGGTG	3060
OY	22463	GCGGCAGATGAGTTACATATACCCCAACAGCAGAGTTGCGGGCGGGTCCGCTCATGAGAC	22522
Db	3061	GCGGCAGATGAGTTACATATACCCCAACAGCAGAGTTGCGGGCGGGTCCGCTCATGAGAC	3120
OY	22523	CCATTAAGAAAGCATAATCACTACACACCGGAACACCGCAAAAAAACGACACGCAAAAA	22582
Db	3121	CCATTAAGAAAGCATAATCACTACACACCGGAACACCGCAAAAAAACGACACGCAAAAA	3180
OY	22583	GGCCCGCTATGTTGATGACAAAAACACAAAAACAAGACGGGGGTGCGTCTGCGTGGCTTGCACACAG	22642
Db	3181	GGCCCGCTATGTTGATGACAAAAACACAAAAACAAGACGGGGGTGCGTCTGCGTGGCTTGCACACAG	3240
OY	22643	CGCCACGCTCGCCGTGCTGGGCCACGGGTGACGGGCTCCATTAATACCCGCGGCCCGGGC	22702
Db	3241	CGCCACGCTCGCCGTGCTGGGCCACGGGTGACGGGCTCCATTAATACCCGCGGCCCGGGC	3300
OY	22703	CCGCGCTGACGGAAACCAAGGCGTGGTTAAGCCACTGACGACGTGCTCCGTCACAGATG	22762
Db	3301	CCGCGCTGACGGAAACCAAGGCGTGGTTAAGCCACTGACGACGTGCTCCGTCACAGATG	3360
OY	22763	TGGCATTCGAGTCCCAAAAACGGGCGTGTACTACAGGCGCGGCCCGGGGTTCAAAAGAAC	22822
Db	3361	TGGCATTCGAGTCCCAAAAACGGGCGTGTACTACAGGCGCGGCCCGGGGTTCAAAAGAAC	3420
OY	22823	GGGGATCCCCCAACAGGTAAAAAGCTTTTGTGCCAAGCAGAAAGCCAACAGCAACCGAA	22882
Db	3421	GGGGATCCCCCAACAGGTAAAAAGCTTTTGTGCCAAGCAGAAAGCCAACAGCAACCGAA	3480
OY	22883	AGGAATCTCCAAAACAAGCAAGGTCCTCGTGGCGGCGATTAACGGAAAAATTTCCCTCACCC	22942
Db	3481	AGGAATCTCCAAAACAAGCAAGGTCCTCGTGGCGGCGATTAACGGAAAAATTTCCCTCACCC	3540
OY	22943	TAAACACACGCGCGCGGTAAACGTGTTAAACACAGCAATCTTCCTGAGCGTGGTTTAT	23002
Db	3541	TAAACACACGCGCGCGGTAAACGTGTTAAACACAGCAATCTTCCTGAGCGTGGTTTAT	3600
OY	23003	AAAAACACACAAGGTTGTAAATTTTCGCGGGGCGCTTTGGGCGCCCGCGCTGTGGGGGTGGC	23062
Db	3601	AAAAACACACAAGGTTGTAAATTTTCGCGGGGCGCTTTGGGCGCCCGCGCTGTGGGGGTGGC	3660
OY	23063	TTGTCTCGTGTGGTTGCAATCACACCCCGCTGCGGAAAAACAGGGCAACACCCCG	23122

Db 3661 TTGCTGCTGTTGTTGTCGCAATCAACACCCCGCTGCCGGAACAGGCAACACCCCC 3720
Oy 23123 TGCGCTAGTTTTTTAAACCTTAACACCGGCGAGGAGGAGGAAGAGGGTGGCGCTAA 23182
Db 3721 TGCGCTAGTTTTTTAAACCTTAACACCGGCGAGGAGGAGGAGGAAGAGGGTGGCGCTAA 3780
Oy 23183 ATGGGCTGTTAGACGACCAACCGCA 23206
Db 3781 ATGGGCTGTTAGACGACCAACCGCA 3804
RESULT 5
AF159033 475 bp DNA linear VRL 28-APR-2000
LOCUS Macaque gamma virus strain Macaca mulatta gamma virus DNA
DEFINITION polymerase (pol) gene, partial cds.
ACCESSION AF159033
VERSION AF159033.1 GI:6671074
KEYWORDS
SOURCE Macaque gamma virus
ORGANISM Macaque gamma virus
VIRUSES; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE 1 (bases 1 to 475)
AUTHORS Strand,K., Harper,E., Thormahlen,S., Thoulless,M.E., Tsai,C.,
Rose,T. and Bosch,M.L.
TITLE Two distinct lineages of macaque gamma herpesviruses related to the
J. Clin. Virol. 16 (3), 253-269 (2000)
MEDLINE 20204465
PUBMED 10738144
REFERENCE 2 (bases 1 to 475)
AUTHORS Strand,K.B. and Bosch,M.L.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
357238, Seattle, WA 98125, USA
FEATURES
source
1. 475
/organism="Macaque gamma virus"
/mol_type="genomic DNA"
/strain="Macaque mulatta gamma virus"
/db_xref="taxon:111468"
<1..>475
/gene="pol"
<1..>475
/gene="pol"
/codon_start=2
/product="DNA polymerase"
/protein_id="AAF23083.1"
/db_xref="GI:6671075"
/translation="SITQAHNLICVSTMIGHRDILHAPNTLPDQVETEVLSGGPVHFVK
KHKRESILGRILTYWLEKRRIRRTLAACDDPSKTLIDKQOLAIKYTCNAYVCFGV
ASGLPCINIAIEVTLTKRTMLEMSKSYVALTTEDLRTLRIGREVTARHGAREFV"
BASE COUNT 110 a 141 c 143 g 81 t
ORIGIN
Query Match 1.2%; Score 475; DB 1; Length 475;
Best Local Similarity 100.0%; Pred. NO. 4.8e-268;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 181 AGAAAGGAGGCGATCCGCGACCCCTGGCGCGGTGCATGACCCGCTGCTAATAAAC 240
Oy 16143 CATCTTAGATTAACAACAGCTGGCCATCAACGATCATGTAAACGGGTTTACGGGTTCAC 16202
Db 241 CATCTTAGATTAACAACAGCTGGCCATCAACGATCATGTAAACGGGTTTACGGGTTCAC 300
Oy 16203 CGGGGTGGCCAGCGGCTCTCCATGATTAACATAGCGGAACCGGAGCTCCGCGG 16262
Db 301 CGGGGTGGCCAGCGGCTCTCCATGATTAACATAGCGGAACCGGAGCTCCGCGG 360
Oy 16263 GCGCAGATGCTGAGATGTCAAAGTCTTACGTGAGGCGCTGACGAGGAGGACTTCG 16322
Db 361 GCGCAGATGCTGAGATGTCAAAGTCTTACGTGAGGCGCTGACGAGGAGGACTTCG 420
Oy 16323 AACGCTCTCGGTGCGGACGAGTGACCGCCGTCACGCGCGGCTTCCGCTGCTC 16377
Db 421 AACGCTCTCGGTGCGGACGAGTGACCGCCGTCACGCGCGGCTTCCGCTGCTC 475

RESULT 6
AF159041 395 bp DNA linear VRL 28-APR-2000
LOCUS Macaque gamma virus strain Macaca mulatta gamma virus glycoprotein
DEFINITION B (gB) gene, partial cds.
ACCESSION AF159041
VERSION AF159041.1 GI:6671090
KEYWORDS
SOURCE Macaque gamma virus
ORGANISM Macaque gamma virus
VIRUSES; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE 1 (bases 1 to 395)
AUTHORS Strand,K., Harper,E., Thormahlen,S., Thoulless,M.E., Tsai,C.,
Rose,T. and Bosch,M.L.
TITLE Two distinct lineages of macaque gamma herpesviruses related to the
J. Clin. Virol. 16 (3), 253-269 (2000)
MEDLINE 20204465
PUBMED 10738144
REFERENCE 2 (bases 1 to 395)
AUTHORS Strand,K.B. and Bosch,M.L.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
357238, Seattle, WA 98125, USA
FEATURES
source
1. 395
/organism="Macaque gamma virus"
/mol_type="genomic DNA"
/strain="Macaque mulatta gamma virus"
/db_xref="taxon:111468"
<1..>395
/gene="gB"
<1..>395
/gene="gB"
/codon_start=3
/product="glycoprotein B"
/protein_id="AAF23091.1"
/db_xref="GI:6671091"
/translation="GTEDEKTHQESILVAFKKNIIVPHIFKVRKRVATSVTVRGATE
TAVYGEQEVIRPVQYEINHDFTYQCFSSRVVAVNGIVNTYTRDPTNCFVFLQPYE
GLNDIDRYSOPPLVYTPGMFPEIYVR"
BASE COUNT 106 a 113 c 108 g 68 t
ORIGIN

Query Match 0.8%; Score 331; DB 1; Length 395;
Best Local Similarity 99.7%; Pred. NO. 3.3e-183;
Matches 381; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 11759 CGGACCGGAGGACAGACGACCAAGAGCATCTGATGCTTTTAAATAATATG 11818
Db 1 CGGACCGGAGGACAGACGACCAAGAGCATCTGATGCTTTTAAATAATATG 60

QY 11819 TCCCGACATCTTTAAAGTCAGACGCTACCGCAGAGTGGCCACCTGGTGGACCGTCTATC 11878
|||||
Db 61 TCCCGACATCTTTAAAGTCAGACGCTACCGCAGAGTGGCCACCTGGTGGACCGTCTATC 11878
11879 GAGGGTGCACGACGACCGCGGTGACCGGACCAAGAGTGCATCCGACCGGTGGCCAGT 11938
|||||
Db 121 GAGGGTGCACGACGACCGCGGTGACCGGACCAAGAGTGCATCCGACCGGTGGCCAGT 1180
11939 ACGAGATCAACACATGACGACGACCTACCACTGTTTCAGTCCATCGCGTAAACGTCA 11998
181 ACGAGATCAACACATGACGACGACCTACCACTGTTTCAGTCCATCGCGTAAACGTCA 240
QY 11999 ACGGATAGTAAACCTACAGGACGAGGACTTCACTAAACAGACCGGTGTTTCAGC 12058
|||||
Db 241 ACGGATAGTAAACCTACAGGACGAGGACTTCACTAAACAGACCGGTGTTTCAGC 300
QY 12059 CGGTGAGGAGGCTGACGATACATCAGCAGTACTTCACTAGCGGCTGTACACGA 12118
|||||
Db 301 CGGTGAGGAGGCTGACGATACATCAGCAGTACTTCACTAGCGGCTGTACACGA 360
12119 CACCGGATGTTTCCGGGAAT 12140
|||||
Db 361 CACCGGATGTTTCCGGGAAT 382
RESULT 7
AF159040 320 bp DNA linear VRL 28-APR-2000
LOCUS Macaque gamma virus strain Macaque fascicularis gamma virus
DEFINITION glycoprotein B (gb) gene, partial cds.
ACCESSION AF159040
VERSION AF159040.1 GI:6671088
KEYWORDS
SOURCE Macaque gamma virus
ORGANISM Macaque gamma virus.
REFERENCE 1 (bases 1 to 320)
AUTHORS Gamaherpesvirinae: Rhadinovirus.
TITLE Strand, K., Harper, E., Thormahlen, S., Thoulless, M.E., Tsai, C.,
Rose, T. and Bosch, M.L.
Two distinct lineages of macaque gamma herpesviruses related to the
Kaposi's sarcoma associated herpesvirus
J. Clin. Virol. 16 (3), 253-269 (2000)
JOURNAL
MEDLINE 20204465
PUBMED 10738144
REFERENCE 2 (bases 1 to 320)
AUTHORS Strand, K.B. and Bosch, M.L.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
357238, Seattle, WA 98125, USA
FEATURES
source
1. 320
/organism="Macaque gamma virus"
/mol_type="genomic DNA"
/strain="Macaque fascicularis gamma virus"
/db_xref="taxon:111468"
1. .>320
/gene="gb"
1. .>320
/gene="gb"
/codon_start=3
/product="glycoprotein B"
/protein_id="AAF23090.1"
/db_xref="GI:6671088"
translation="VRRYKVAIVSVTVRKGWETAVTGKOEVRVPEVPEIHHMDT
OCESMRNVNVMVINTYDRDFTNQTFLQPEGLDNIQRTFSQPVLYTTGMPGI
YRVR"
BASE COUNT 78 a 96 c 92 g 54 t
ORIGIN
Query Match 0.3%; Score 106; DB 1; Length 320;
Best Local Similarity 99.4%; Pred. No. 1.2e-50;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11834 AGGTGACAGCGTACCGCAAGGTGGCCACCTCGGTGACCGTCTATGAGGGTGGACCGAGA 11893
|||||
Db 1 AGGTGACAGCGTACCGCAAGGTGGCCACCTCGGTGACCGTCTATGAGGGTGGACCGAGA 60
QY 11894 CCGCGGTGACCGGCAAGAGGTGATCGACCGGCTGGCGAGTACGAGTACCAACCA 11953
|||||
Db 61 CCGCGGTGACCGGCAAGAGGTGATCGACCGGCTGGCGAGTACGAGTACCAACCA 120
QY 11954 TGGACAGCAGCTACAGTGTTCAGCTCCATCGCGGT 11990
|||||
Db 121 TGGACAGCAGCTACAGTGTTCAGCTCCATCGCGGT 157
RESULT 8
AF204167 2708 bp DNA linear VRL 04-JUL-2000
LOCUS Macaca nemestrina rhadinovirus 2 DNA polymerase and ORF 10-like
DEFINITION protein genes, partial cds.
ACCESSION AF204167
VERSION AF204167.1 GI:8925895
KEYWORDS
SOURCE Macaca nemestrina rhadinovirus 2
ORGANISM Macaca nemestrina rhadinovirus 2
REFERENCE 1 (bases 1 to 2708)
AUTHORS Gamaherpesvirinae: Rhadinovirus.
TITLE Schultz, E.R., Rankin, G.W., Jr., Blanc, M.P., Raden, B.W., Tsai, C.C.
and Rose, T.M.
Characterization of two divergent lineages of macaque
rhadinoviruses related to Kaposi's sarcoma-associated herpesvirus
J. Virol. 74 (10), 4919-4928 (2000)
JOURNAL
MEDLINE 20240083
PUBMED 10775636
REFERENCE 2 (bases 1 to 2708)
AUTHORS Rose, T.M.
TITLE Direct Submission
JOURNAL Submitted (12-NOV-1999) Pathobiology, School of Public Health and
Community Medicine, University of Washington, Seattle, WA 98195,
USA
FEATURES
source
1. 2708
/organism="Macaca nemestrina rhadinovirus 2"
/mol_type="genomic DNA"
-/isolate="Mne442N"
/db_xref="taxon:123630"
1. .2589
/note="MneRV-2"
/note="similar to rhesus rhadinovirus ORF 9"
/codon_start=1
/product="DNA polymerase"
/protein_id="AAE81664.1"
/db_xref="GI:8925895"
translation="ROOYFYKAVPSGVNTHVLQALKNTRAGACGSPRRVRRI
LKYTVAEHPYETITLSSGPMISTISDLVAVCGGPPSNDVAVRPVLDHETFGW
TCSRATPELRLARDAKIALDEFDCSWEDSVQADGRNDMPYRIMADIEICVGTFPCA
TRDCDAVIOISCVFYTRDGATPPNVLEVSQCDPIRDTVLEPSEEDMIVSFFAM
LRDEFVDELGTGINSFNDLPYLIAASOVYNQLMEYTKIKGSIFFEVHEPAGAGGF
MRSVKIKIAGIVPDMYOVCREKLSIDYKIDYAROCIGKEDVSKDIPERS
GSAGRAKGVSVCMDSVILMKMFMIHVEISELAKTAKIARGLVDGGOOLRVFSC
LLEAARENFILPVTPEGSGGTGATVINIPGTYDEPVLVVDASLPSITQAHNL
CYSTMIGHRDHLHPTLPDDYETVLSGGPVHEVKKHRESLRLTLVLEKRAI
RRTLAACDDPSLKLILDKOOLAIKVTNAVVGTVASGLPCINIAETVLKGRRL
EMSKSYVALIVSDLERIGREVTAGPAKFEVYVGDPSLEIACGVPADAVSAFCD
DLAARTADLPPEPKILEAEKEFKLLLTLLKRYIGVLLNDKMWKGVDLIKTACKF
VOEGRATLIDYIHDEPVEYKAARILCKKRPRAVVEEGIPRGTIKVEYVLMNSYLDIRN
DAVPLEQITFTELSRPVCDYKTTNLPHTYIQKLASCBEIPYHDXNIPYFVNDAR
TLDLAHPDPVTRORHRIPIAVDLYFDKLVRAANILOCLEGNADTTVALINFLNV
PKYIFS"
2683. .>2708
/note="similar to rhesus rhadinovirus ORF 10"
/codon_start=1
/product="ORF 10-like protein"

```

BASE COUNT      559 a      852 c      811 g      486 t
ORIGIN
Query Match      0.2%; Score 80; DB 1; Length 2708;
Best Local Similarity 100.0%; Pred. No. 3.2e-35;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15703 CAGCCGAGCGCGCTCTGACGAGCGCCACACAGCTCCGCGTCTCTCGCTCTGAG 15762
D 1126 CAGCCGAGCGCGCTCTGACGAGCGCCACACAGCTCCGCGTCTCTCGCTCTGAG 1185
OY 15763 GCGCGGCGCAGGAGAACTT 15782
D 1186 GCGCGGCGCAGGAGAACTT 1205

RESULT 9
AF159031
LOCUS      475 bp      DNA      linear      VRL 28-APR-2000
DEFINITION Macaque gamma virus strain Macaca nemestrina gamma virus DNA
ACCESSION AF159031
VERSION AF159031.1 GI:6671070
KEYWORDS
SOURCE Macaque gamma virus
ORGANISM Macaque gamma virus
VIRUSES: dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE 1 (bases 1 to 475)
AUTHORS Strand,K., Harper,E., Thormahlen,S., Thoulless,M.E., Tsai,C.,
TITLE Two distinct lineages of macaque gamma herpesviruses related to the
JOURNAL Kaposi's sarcoma associated herpesvirus
MEDLINE J. Clin. Virol. 16 (3), 253-269 (2000)
20204465
PUBMED 10738144
2 (bases 1 to 475)
AUTHORS Strand,K.B. and Bosch,M.L.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
357238, Seattle, WA 98125, USA
FEATURES
SOURCE Location/Qualifiers
1. 475
/organism="Maque gamma virus"
/mol_type="genomic DNA"
/strain="Macaca nemestrina gamma virus"
/db_xref="taxon:111468"
<1..>475
/gene="pol"
<1..>475
/gene="pol"
<1..>475
/codon_start=2
/product="DNA polymerase"
/protein_id="AAF23081.1"
/db_xref="GI:6671071"
/translation="STIOAHMLCYSTIHGRDLHPTLPDPDYETVLSGGPVHFK
KHKRESLLGRLLTWLEKRAIRIRTLACDPSLKTILDKQALAIKVCNAVYGTGV
ASGSLPQINIAETVTLGRRTMLEMSKYVEALIVSDLRERLGRVETAGPDAKFRV"
BASE COUNT      100 a      147 c      152 g      76 t
ORIGIN
Query Match      0.2%; Score 71; DB 1; Length 475;
Best Local Similarity 100.0%; Pred. No. 5.2e-30;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15903 GAGCATATCCAGCGGACACACTGTGCTACTCCACATGATACAGGAGAGACCTGCA 15962
D 1 GAGCATATCCAGCGGACACACTGTGCTACTCCACATGATACAGGAGAGACCTGCA 60
OY 15963 CCTGACCCCA 15973

```

```

Db 61 CCTGACCCCA 71
|||||
RESULT 10
AF159034
LOCUS      336 bp      DNA      linear      VRL 28-APR-2000
DEFINITION Macaque gamma virus strain Macaca nemestrina 116 gamma virus DNA
ACCESSION AF159034
VERSION AF159034.1 GI:6671076
KEYWORDS
SOURCE Macaque gamma virus
ORGANISM Macaque gamma virus
VIRUSES: dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE 1 (bases 1 to 336)
AUTHORS Strand,K., Harper,E., Thormahlen,S., Thoulless,M.E., Tsai,C.,
TITLE Two distinct lineages of macaque gamma herpesviruses related to the
JOURNAL Kaposi's sarcoma associated herpesvirus
MEDLINE J. Clin. Virol. 16 (3), 253-269 (2000)
20204465
PUBMED 10738144
2 (bases 1 to 336)
REFERENCE Strand,K.B. and Bosch,M.L.
AUTHORS Direct Submission
JOURNAL Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
357238, Seattle, WA 98125, USA
FEATURES
SOURCE Location/Qualifiers
1. 336
/organism="Maque gamma virus"
/mol_type="genomic DNA"
/strain="Macaca nemestrina 116 gamma virus"
/db_xref="taxon:111468"
<1..>336
/gene="pol"
<1..>336
/gene="pol"
<1..>336
/codon_start=2
/product="DNA polymerase"
/protein_id="AAF23084.1"
/db_xref="GI:6671077"
/translation="TMIHGRDLHPTLPDPDYETVLSGGPVHFKHKRESLLGR
LTVWLEKRAIRIRTLACDPSLKTILDKQALAIKVCNAVYGTGVAAGSLPQINIA
ETVLRGR"
BASE COUNT      75 a      103 c      105 g      53 t
ORIGIN
Query Match      0.1%; Score 56; DB 1; Length 336;
Best Local Similarity 100.0%; Pred. No. 3.4e-21;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15976 CTGACGCGGACGACGACGACGCTGCTGAGCGGACGCGTACATTGTG 16031
D 41 CTGACGCGGACGACGACGACGCTGCTGAGCGGACGCGGTACATTGTG 96

RESULT 11
AF159032
LOCUS      475 bp      DNA      linear      VRL 28-APR-2000
DEFINITION Macaque gamma virus strain Macaca fascicularis gamma virus DNA
ACCESSION AF159032
VERSION AF159032.1 GI:6671072
KEYWORDS
SOURCE Macaque gamma virus
ORGANISM Macaque gamma virus
VIRUSES: dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE 1 (bases 1 to 475)
AUTHORS Strand,K., Harper,E., Thormahlen,S., Thoulless,M.E., Tsai,C.,

```

TITLE Two distinct lineages of macaque gamma herpesviruses related to the
Kapoli's sarcoma associated herpesvirus
J. Clin. Virol. 16 (3), 253-269 (2000)
MEDLINE 20204465
PUBMED 10738144
REFERENCE 2 (bases 1 to 475)
AUTHORS Strand, K.B. and Bosch, M.L.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
357238, Seattle, WA 98125, USA
FEATURES
source Location/Qualifiers
1..475
/organism="Macaque gamma virus"
/mol_type="genomic DNA"
/strain="Macaque fascicularis gamma virus"
/db_xref="taxon:111468"
<1..>475
/gene="pol"
<1..>475
/gene="pol"
/codon_start=2
/product="DNA polymerase"
/protein_id="AA023082.1"
/db_xref="GI:6671073"
/translation="STIDAHNLCTSTMTHGDDLHLPITLTPDDYETFPVLSGGPVHFKV
KHKRESLIGRLTVMLEKRRIRLTLACDDPSLTKITLKDQDLAKVTCNAVYGFVGV
ASGLPCINIAETVTLRGRTMLEMSKSVLEATLTDLRGLRGVYTAGHGAFRVV"
BASE COUNT 99 a 144 c 152 g 80 t
ORIGIN
Query Match 0.1%; Score 50; DB 1; Length 475;
Best Local Similarity 100.0%; Pred. No. 1.2e-17;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 15903 GAGCATTCACGCGGACACCTGCTGCTACCTCAGCATGATACACGGAC 15952
DB 1 GAGCATTCACGCGGACACCTGCTGCTACCTCAGCATGATACACGGAC 50
RESULT 12
AF159036 336 bp DNA linear VRL 28-APR-2000
LOCUS Macaque gamma virus strain Macaca fascicularis 037 gamma virus DNA
DEFINITION Macaque gamma virus strain Macaca fascicularis 037 gamma virus DNA
ACCESSION AF159036
VERSION AF159036.1 GI:6671080
KEYWORDS
SOURCE Macaque gamma virus
ORGANISM Macaque gamma virus
VIRUSES: dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE 1 (bases 1 to 336)
AUTHORS Strand, K., Harper, E., Thormahlen, S., Thouless, M.E., Tsai, C.,
Rose, T. and Bosch, M.L.
TITLE Two distinct lineages of macaque gamma herpesviruses related to the
Kapoli's sarcoma associated herpesvirus
J. Clin. Virol. 16 (3), 253-269 (2000)
MEDLINE 20204465
PUBMED 10738144
REFERENCE 2 (bases 1 to 336)
AUTHORS Strand, K.B. and Bosch, M.L.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
357238, Seattle, WA 98125, USA
FEATURES
source Location/Qualifiers
1..336
/organism="Macaque gamma virus"
/mol_type="genomic DNA"
/strain="Macaque fascicularis 037 gamma virus"
/db_xref="taxon:111468"
<1..>336
/gene="pol"
<1..>336
/gene="pol"

/gene="pol"
/codon_start=2
/product="DNA polymerase"
/protein_id="AA023086.1"
/db_xref="GI:6671081"
/translation="TWIHGRDLHLPITLTPDDYETFPVLSGGPVHFKHKRESLIGRL
LTVMLEKRRIRLTLACDDPSLTKITLKDQDLAKVTCNAVYGFVGVASGLPCINIA
ETVTLRGRT"
BASE COUNT 75 a 101 c 107 g 53 t
ORIGIN
Query Match 0.1%; Score 48; DB 1; Length 336;
Best Local Similarity 100.0%; Pred. No. 1.8e-16;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 15975 CCTGACGCCGCGAGCTACGACGCTGCTGCTGACGCGGACCGGT 16022
DB 40 CCTGACGCCGCGAGCTACGACGCTGCTGCTGACGCGGACCGGT 87
RESULT 13
AF159037 336 bp DNA linear VRL 28-APR-2000
LOCUS Macaque gamma virus strain Macaca fascicularis 040 gamma virus DNA
DEFINITION Macaque gamma virus strain Macaca fascicularis 040 gamma virus DNA
ACCESSION AF159037
VERSION AF159037.1 GI:6671082
KEYWORDS
SOURCE Macaque gamma virus
ORGANISM Macaque gamma virus
VIRUSES: dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE 1 (bases 1 to 336)
AUTHORS Strand, K., Harper, E., Thormahlen, S., Thouless, M.E., Tsai, C.,
Rose, T. and Bosch, M.L.
TITLE Two distinct lineages of macaque gamma herpesviruses related to the
Kapoli's sarcoma associated herpesvirus
J. Clin. Virol. 16 (3), 253-269 (2000)
MEDLINE 20204465
PUBMED 10738144
REFERENCE 2 (bases 1 to 336)
AUTHORS Strand, K.B. and Bosch, M.L.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
357238, Seattle, WA 98125, USA
FEATURES
source Location/Qualifiers
1..336
/organism="Macaque gamma virus"
/mol_type="genomic DNA"
/strain="Macaque fascicularis 040 gamma virus"
/db_xref="taxon:111468"
<1..>336
/gene="pol"
<1..>336
/gene="pol"
/codon_start=2
/product="DNA polymerase"
/protein_id="AA023087.1"
/db_xref="GI:6671083"
/translation="TWIHGRDLHLPITLTPDDYETFPVLSGGPVHFKHKRESLIGRL
LTVMLEKRRIRLTLACDDPSLTKITLKDQDLAKVTCNAVYGFVGVASGLPCINIA
ETVTLRGRT"
BASE COUNT 75 a 101 c 107 g 53 t
ORIGIN
Query Match 0.1%; Score 48; DB 1; Length 336;
Best Local Similarity 100.0%; Pred. No. 1.8e-16;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 15975 CCTGACGCCGCGAGCTACGACGCTGCTGCTGACGCGGACCGGT 16022
DB 40 CCTGACGCCGCGAGCTACGACGCTGCTGCTGACGCGGACCGGT 87

RESULT 14
AF159035
LOCUS
DEFINITION Macaque gamma virus strain Macaca nemestrina 139 gamma virus DNA
ACCESSION AF159035
VERSION AF159035.1 GI:6671078
KEYWORDS
SOURCE Macaque gamma virus
ORGANISM Macaque gamma virus
REFERENCE
AUTHORS Gammaherpesvirinae; Rhadinovirus.
1 (bases 1 to 336)
Strand, K., Harper, E., Thormalen, S., Thoulless, M.E., Tsai, C.,
Rose, T., and Bosch, M.L.
Two distinct lineages of macaque gamma herpesviruses related to the
Kaposi's sarcoma associated herpesvirus
J. Clin. Virol. 16 (3), 253-269 (2000)
20204465
10738144
2 (bases 1 to 336)
Strand, K.B. and Bosch, M.L.
Direct Submission
Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
357238, Seattle, WA 98125, USA
JOURNAL MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
FEATURES
source
1. .336
Location/Qualifiers
/organism="Maque gamma virus"
/mol_type="genomic DNA"
/strain="Macaque nemestrina 139 gamma virus"
/db_xref="taxon:111468"
1. .>336
/gene="pol"
<1. .>336
/gene="pol"
/codon_start=2
/product="DNA polymerase"
/protein_id="AA23085.1"
/db_xref="GI:6671078"
/translation="TMHGRDLHPTLPDDYETVYLSGSPVHFVKKHRESILGLT
LTYMLEKRRRAIRRTLAACDPSLKTITLDKQDLAIKVCNAVYGTGASGLPCINIA
ETVTLRRT"
BASE COUNT 74 a 103 c 106 g 53 t
ORIGIN
Query Match 0.1%; Score 47; DB 1; Length 336;
Best Local Similarity 100.0%; Pred. No. 6.9e-16;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 15976 CTGACGCGGAGACGACGACGCTGCTGAGCGGAGCGCGT 16022
Db 41 CTGACGCGGAGACGACGACGCTGCTGAGCGGAGCGCGT 87

RESULT 15
SH1DNAPOLA
LOCUS
DEFINITION Pseudorabies virus DNA polymerase gene, partial cds.
ACCESSION L24487
VERSION L24487.1 GI:438894
KEYWORDS DNA polymerase.
SOURCE Pseudorabies virus
ORGANISM Pseudorabies virus
REFERENCE
AUTHORS Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicelloviruses.
1 (bases 1 to 3144)
Bertomme, H., Monahan, S.J., Parris, D.S., Jacquemont, B. and
Epstein, A.L.
Cloning, sequencing, and functional characterization of the two
subunits of the pseudorabies virus DNA polymerase holoenzyme:
evidence for specificity of interaction
J. Virol. 69 (5), 2811-2818 (1995)

MEDLINE 95222727
PUBMED 7707503
COMMENT Original
Kaplan) DNA.
FEATURES
source
1. .3144
Location/Qualifiers
/organism="Pseudorabies virus"
/mol_type="genomic DNA"
/isolate="Kaplan"
/db_xref="taxon:10345"
1. .>3144
/codon_start=1
/product="DNA polymerase"
/protein_id="AA474383.1"
/db_xref="GI:438895"
CDS
/translation="MAROGSVYTRLSSEKFIAPRCIDAPEDQGVHYGTIAREPTVYC
GGATPILRGEPTPRRVAAMMEGAPDEPVPSPREPRFVYDIVESTEVASDPFRPKT
VVTLLGASGKRVAVHYGVRRHFFLGKAEADAAALVASAEQALRALSAAGAARPL
GPADVDARVYDAAPVYVYDAPRRPFYEVSSNSGLVHNLRETVCAGLVTHEAGVATT
RLLDHDLPSFGVRLRPPGAGERVYVLRHRLSSDVEVNTCTPLNARDDEGPPDYK
LLCFEDICRAGDDAAPPAENPEDLVIOISCLYSIATOREHTLFLFSGSDDDPA
VTVLEPDSREELLIAVTVLTKOYAPPAATGYNITIPMAVHFRTLVVGLADGCR
FNRGGQPRVYDAGONSQRKSKYKINCLVSLDMYAVADKLKLPSTYKLVABEALGE
RKLDLDYKDIPTYAAGPRERGVIGRCVODSALVGLFKEFLPHLELSAVARLANIT
LARAIVDGOQIRVETCLKLAGSKGFLVLPKRRALADEDSGGGKYLEPDSGFVY
DPVLVDLPSLPSIIQAHNLCTFTLLARPAQRLDEFSAFEVNGERLYFVHAGVRE
SLSTILRDLAMRKARIRARIPTSAPAEVLLDKQAAIRVGCNSVYGTGVANGLLP
CLPYAAVTITIGRDMVATRDYVOTRATRELBELRDIPARPPAGEIVAVRYVYGTDSV
FTRSGIAYDVCEBGLMARTTRDLPFRPIKECKTRRLILTKKTIIGVING
KMLMGVDIVRKNNCAFINAVARLVLDLFEGDEVSAANAATIAAPARMLERVLPNG
FAAFGRVLAHAHARVAGAGLVDVADPMTAELSRPPAYSVTRLPHTVYVHAKLMRHG
EVPVSKEVSVYIIAPTPEARDGAVRPGKLVSDLAEDPAVYVHAGVLENT
YFSSHLSLSTSVTFKALFNGDRTKTERLLKRFIPETAPGDAPFEHFAALTGCGGS
LQTLRTFTCTPAAPRS"
BASE COUNT 463 a 1172 c 1050 g 459 t
ORIGIN
Query Match 0.1%; Score 46; DB 1; Length 3144;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 15886 TTTCGACGCTGTACCGAGCATCATCCAGCGCACAACCTGTGCT 15931
Db 1720 TTTCGACGCTGTACCGAGCATCATCCAGCGCACAACCTGTGCT 1765

Search completed: September 25, 2003, 11:53:05
Job time : 11973 secs

THIS PAGE BLANK (USPTO)